

SEQUENCE LISTING

<110> Zyskind, Judith
Ohlsen, Kari L.
Trawick, John
Forsyth, R. Allyn
Froelich, Jamie M.
Carr, Grant J.
Yamamoto, Robert T.
Xu, H. Howard

<120> GENES IDENTIFIED AS REQUIRED FOR PROLIFERATION IN
ESCHERICHIA COLI

<130> ELITRA.001DV1

<150> 09/492,709

<151> 2000-01-27

<150> 60/117,405

<151> 1999-01-27

<160> 485

<170> FastSEQ for Windows Version 3.0

<210> 1

<211> 159

<212> DNA

<213> E. Coli

<400> 1

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atcaccagca	gatgaaataa	cgataaccag	aacaacgcct	tatagcgttg	agtttgcgag	120
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<211> 696

<212> DNA

<213> E. Coli

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<222> (1)...(696)

<223> n = A,T,C or G

<400> 2

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gtcacctact	caaacgtgga	accgagcgat	ttcgttcaga	ccttctcacg	ccgtaatggt	180
ggggaagcga	ccagcggatt	ctttgaagtg	ccgaaaaacg	aaaccaaaga	aaatggaatt	240
cgtctttccg	agcgtaaaga	gacactgggt	gatgtgacgc	accgcattct	gacagtgccg	300
attgcgcagg	atcaggtggg	gatgtattac	cagcagccag	ggcaacaact	ggcaacctgg	360

attgttcctc	cgggacaata	cttcatgatg	ggcgacaacc	gcgacaacag	cgcgacagc	420
cgttactggg	gctttgtgcc	ngaagcgaat	ctggtcggtc	nggcaacggc	tatctggatg	480
aacttcgata	accaagaagg	cgaatggccg	aatggctctg	cctaantcgc	attggcgnnt	540
ccnttaatan	ccacttcctt	cncctttgtcc	ccttatggca	acacttaatt	tattntaaan	600
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ggcctccagt	tgcccgnccc	aaacactttg	gncccc			696

<210> 3
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 <212> DNA
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<400> 3						
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acgtaagcgg	atggagtggc	cggaacctc	atagtaccg	cccaccagt	ggcctgcac	180
gctttgtagc	gtacgcgcgg	cattggcaat	aagattcaga	tactcagact	cttccggggc	240
cttcgccagc	ataaaagagg	aggatgctcg	cgtatgcagc	aactgctcca	gcgcaaattg	300
cagccgcggg	tgagtatcac	tgaataaagg	atcgttttcg	tcaatcaaat	gtggctgagc	360
aaatatttcc	tgatagctat	cggatcacgg	aaccagggtca	cgccatgcaa	gtttcgtaat	420
ggtcaaagtt	gatgtttttt	agtctgttgt	caaagccgcn	attataccng	taaccggcac	480
tacagcacac	gtagaaagca	cccagacaata	ctcctggcat	gggcggttaa	gtcacagga	540
tggagatctt	ttcttcactg	gcctaaaaag	ctgatattct	gtaaagagtt	acacngtaac	600
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gaaagtatct	ggttaagaag	c				681

<210> 4
 <211> 289
 <212> DNA
 <213> E. Coli

<400> 4						
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tacttaacgg	agaaccatta	agccttagga	cgcttcacgc	catacttgga	acgagcctgc	180
ttacggtctt	taacgccgga	gcagtcaagc	gcaccacgta	cggtgtggta	acgaacaccc	240
gggaggtctt	taacacgacc	gtcacggatc	aggatcacgg	agtgtctcct		289

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 <213> E. Coli

<220>
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 <223> n = A,T,C or G

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atatggcccc	ctttttcact	tttatatctg	tgcggtttta	tgccgggcag	atcacatctc	180

cgaggatttt	agaatggctg	aaattaccgc	atccctggta	aaagagctgc	gtgagcgtac	240
tggcgcaggc	atgatggatt	gcaaaaaagc	actgactgaa	gctaacggcg	acatcgagct	300
ggcaatcgaa	aacatgcgta	agtccggtgc	tattaaagca	gcgaaaaaag	caggcaacgt	360
tgctgctgac	ggcgtgatca	aaaccaaaat	cgacggcaac	tacggcatca	ttctggaagt	420
taactgccag	actgacttcg	ttgcaaaaaga	cgctggtttc	caggcgttcg	cagacaaagt	480
tctggacgca	gctgttgctg	gcaaaatcac	tgacgttgaa	gttctgaaag	cacagttcga	540
agaagaacgt	gttgcgctgg	tagcgaaaat	tggtgaaaac	atcaacattc	gccgcgttgc	600
tgcgctggaa	ggcgacgttc	tgggttctta	tcagcacggg	gcgcgtatcg	gccgttctgg	660
ttgctgctaa	aagcgctgac	gaagaactgg	ttaaacacat	cgttttgacc	tttgttgcaa	720
gccaagccag	aattcagaga	aactttccgc	ttcaccggag	gtcccaccca	cangganccc	780
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<210> 6
 <211> 403
 <212> DNA
 <213> E. Coli

<400> 6

caacactatt	ttgttgaccg	gaaaaatggaa	cactttccgc	aatgcctggt	gctatcacgc	60
ttaaaccatt	tcattgcat	ttacacagaa	cggacgtcct	gtcgcagtat	attaagtcgt	120
cgatagaaac	aagcattgaa	aggcacagca	gtagtcaaac	agtgtgaaac	gctactggcg	180
ccttacagcg	caaaaaggct	ggtgactaaa	aagtcaccag	ccatcagcct	gattttctcag	240
gctgcaaccg	gaagggttgg	cttatttaac	ttcaacttca	gcgccagctt	cttcagagc	300
ttttttcagt	gcttctgcgt	cgtctttgct	cacgccttct	ttcagagcag	ccggtgcaga	360
ttctaccagg	tctttagctt	ctttcagacc	caggccagtt	gcg		403

<210> 7
 <211> 149
 <212> DNA
 <213> E. Coli

<400> 7

gagctttttt	cagtgccttct	gcgtcgtctt	tgctcacgcc	ttctttcaga	gcagccggtg	60
cagattctac	caggctcttta	gcttctttca	gaccaggcc	agttgcgcca	cgtactgctt	120
tgataacagc	aactttgtta	gcgcccagca				149

<210> 8
 <211> 742
 <212> DNA
 <213> E. Coli

<220>

<221> misc_feature
 <222> (1)...(742)
 <223> n = A,T,C or G

<400> 8

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ggacgtcctg	tcgcagtata	ttaagtcgtc	gatagaaa	agcattgaaa	ggcacagcag	180
tagtcaaaca	gtgtgaaacg	ctactggcgc	cttacagcgc	aaaaaggctg	gtgactaaaa	240
agtcaccagc	catcagcctg	atttctcagg	ctgcaaccgg	aagggttggc	ttattttaact	300
tcaacttcag	cgccagcttc	ttccagagct	tttttcagtg	cttctgcgtc	gtctttgctc	360
acgccttctt	tcagagcagc	cggtgcagat	tctaccaggt	ctttagcttc	tttcagaccc	420
aggccagttg	cgccacgtac	tgctttgata	acagcaactt	tgtagcgcc	agcagctttc	480
agaattacgt	cgaattcagt	tntttcttca	gcagcttcaa	ccgggccagc	agctacagct	540
acagcagcag	caagcggaaa	caccgaattt	ttcttccatt	gcagagatca	gttctacaac	600

cgccattac	agacatagct	gcaactgctt	caatgatttt	gatcttttagt	ggatagacat	660
ttaaattgtt	cctgaattat	caagaaataa	gtnttatatg	taagccgaaa	tgcgttaaaa	720
aagataactg	ngattaaagc	ag				742

<210> 9
 <211> 421
 <212> DNA
 <213> E. Coli

<400> 9						
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aaagtcacca	gccatcagcc	tgattttctca	ggctgcaacc	ggaagggttg	gcttatttaa	120
cttcaacttc	agcgccagct	tcttccagag	cttttttcag	tgcttctgcg	tcgtctttgc	180
tcacgccttc	tttcagagca	gccgggtgcag	attctaccag	gtcttttagct	tctttcagac	240
ccaggccagt	tgcgccacgt	actgctttga	taacagcaac	tttgtttagcg	ccagcagctt	300
tcagaattac	gtcgaattca	gttttttctt	cagcagcttc	aaccggggcca	gcagctacag	360
ctacagcagc	agcagcgga	acaccgaatt	tttcttccat	tgagagatc	agttctacaa	420
c						421

<210> 10
 <211> 126
 <212> DNA
 <213> E. Coli

<400> 10						
agagcttttt	tcagtgtctt	tgctgtgtct	ttgtctacgc	cttctttcag	agcagccggt	60
gcagattcta	ccaggtcttt	agcttctttc	agaccaggc	cagttgcgcc	acgtactgct	120
ttgata						126

<210> 11
 <211> 262
 <212> DNA
 <213> E. Coli

<220>
 <221> misc_feature
 <222> (1)...(262)
 <223> n = A,T,C or G

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tctaccaggt	ctttagcttc	tttcagaccc	aggccagttg	cgccacgtac	tgctttgata	180
acagcaactt	tgtttagcgc	agcagctttc	agaattacgt	cgaattcagt	tttttcttca	240
gcagcttcaa	ccgggccagc	ag				262

<210> 12
 <211> 202
 <212> DNA
 <213> E. Coli

<220>
 <221> misc_feature
 <222> (1)...(202)
 <223> n = A,T,C or G

<400> 12

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gtaggtggtg	ttaccggtgn	tcagatccgg	gaagatgaac	acggtagcgc	gacctgcaac	120
cggagagttc	ggcgctttgg	attncgcaac	gtcagccatt	accgcagcgt	cgtactgcag	180
cggaccggcg	atcatcaggt	ca				202

<210> 13
 <211> 261
 <212> DNA
 <213> E. Coli

<400> 13						
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cttttgcccg	gcatgacgcc	gggctttttt	tattattccg	tgacttccag	cgtagtgaag	120
gcaaacttct	cgccatcaaa	tagcccctga	ctggtttagtt	ttagcgcggg	gatcactggc	180
agagaaagaa	acgccatctg	aataaacggc	tcatcgggta	acggaccgca	ttcacggggc	240
gcggctttca	aggcgtcaat	t				261

<210> 14
 <211> 224
 <212> DNA
 <213> E. Coli

<400> 14						
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actcgggaat	tagtataagc	agcgcgagaa	taataatcat	tgtgcaaattg	ctaatttaat	180
taatactatt	taaatattat	tttgagcata	tgacacataag	gttg		224

<210> 15
 <211> 232
 <212> DNA
 <213> E. Coli

<400> 15						
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tgctgatttt	tattattatg	gggaagggtg	tatttatgag	tttcatttat	gccgtaacga	120
caatgaactc	gggaattagt	ataagcagcg	cgagaataat	aatcattgtg	caaagtctaa	180
tttaattaat	actattttaa	tattattttg	agcatatgca	cataagggtg	gg	232

<210> 16
 <211> 212
 <212> DNA
 <213> E. Coli

<400> 16						
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cctcgggtac	ttatgctgat	ttttattatt	atggggaagg	tgttatttat	gagtttcatt	120
tatgccgtaa	cgacaatgaa	ctcgggaatt	agtataagca	gcgcgagaat	aataatcatt	180
gtgcaaatgc	taatttaatt	aatactattt	aa			212

<210> 17
 <211> 433
 <212> DNA
 <213> E. Coli

<400> 17						
ccttgtaa	tatcgcccgt	ggcataaaaa	ctgcgtccaa	acgccgtctt	tgccagcagc	60

caggccataa	atgccaccag	aattatcgtc	aaccaaccaa	ttgctgaaac	gccaaagcagc	120
agcggggcgg	agagctgttt	cagttcggcg	ggtaaccctt	caatccattt	gccgccagtc	180
cacagcaaca	tgatgcctct	gtacaaccct	aacgtgccaa	gggtggcaac	aatggcaggg	240
atcttttagcc	acgcgaccag	gacaccgttg	aaaaatcccg	cgagcaaacc	aagcagtaaa	300
gtcgcgacac	aagcaacagg	tagtgaatat	cctgcgttca	gtaacatccc	caacagcacc	360
gcgcacattc	cggtaatcga	acccactgaa	acatcaatat	tgcgcgtaag	cattaccagc	420
gtcgcgccca	ttg					433

<210> 18
 <211> 658
 <212> DNA
 <213> E. Coli

<400> 18

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tccttccccg	ttgaggacac	cggttgtgca	ggttgacat	acgcttaagt	gacaacccccg	120
ctgcaacgcc	ctctgttatc	aattttctgg	tgacgttttg	cggtatcagt	tttactccgt	180
gactgctctg	ccgccctttt	taaagtgaat	tttgtgatgt	ggtgaatgcg	gctgagcgca	240
cgcggaacag	ttaaaaccaa	aaacagtgtt	atgggtggat	tctctgtatc	cggcgttaat	300
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ggacgcgata	atgaaaacgt	tattaccaa	cgtaatacgc	tctgaagggt	gttttgaaat	420
tggtgtcact	atcagtaacc	cagtatttac	tgaagatgcc	attaacaaga	gaaaacaaga	480
acgggagcta	ttaaataaaa	tatgcattgt	ttcaatgctg	gctcgtttac	gtctgatgcc	540
aaaaggatgt	gcacaatgaa	ttcagcattt	gtgcttgctc	tgacagtttt	tcttgtttcc	600
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<210> 19
 <211> 588
 <212> DNA
 <213> E. Coli

<220>

<221> misc_feature
 <222> (1)...(588)
 <223> n = A,T,C or G

<400> 19

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cacgcggaac	agttaaaacc	aaaaacagtg	ttatgggtgg	attctctgta	tccggcgcta	120
attgttaact	ggttaacgtc	acctggaggc	accaggcact	gcatcacaaa	attcattggt	180
gaggacgcga	taatgaaaac	gttattacca	aacgttaata	cgtctgaagg	ttgttttgaa	240
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gaacgggagc	tattaaataa	aatatgcatt	gtttcaatgc	tggctcgttt	acgtctgatg	360
ccaaaaggat	gtgcacaatg	aattcagcat	ttgtgcttgt	tctgacagtt	tttcttgttt	420
ccggagagcc	agttgatatt	gcagtcagtg	ttcacaggac	aatgcangag	tgtatgactg	480
cagcaacccg	aacagaaaat	tcccggtaac	tgttacccgg	tcgataaagt	tattcaccag	540
gataatatcg	aaatcccggc	aggtctttta	aacagttccg	taataaat		588

<210> 20
 <211> 101
 <212> DNA
 <213> E. Coli

<400> 20

gatccagcaa	gaagatgcgg	ttgtaccgtc	atcacgcaga	tgcgcaaagc	tactcagcaa	60
ctgacctttc	ttcgcaataa	gcacgccatt	agcgtcatag	a		101

<210> 21
 <211> 465
 <212> DNA
 <213> E. Coli

<400> 21
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 cgaggtgcag ttccgccata cccgcgatga tggctctggtt agattcttcg tcagtccata 180
 cacggaaaga cgggtcttct ttagccagac ggcccagagc cagaccatt ttttcctggt 240
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 ccagaatgat cggcgcaccc gggtcacaca ggggtgcacc agtgggttacg tctttcagac 360
 cgatagcagc agcgatgtcg cccgcgcgaa cttctttgat ctcttcacgt ttgttagcgt 420
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<210> 22
 <211> 859
 <212> DNA
 <213> E. Coli

<220>
 <221> misc_feature
 <222> (1)...(859)
 <223> n = A,T,C or G

<400> 22
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 gaatacccat gtctactacc gggtagcctg ccagcggacc tgccttcagc tgctcctgga 180
 tacctttatc aacggccggg atgtattcgc cagggattac accaccttta atgtcgttga 240
 tgaactcgta gcctttcggg tttgaacccg gctccagcgg gtacatgtcg ataacaacat 300
 gaccatactg accacgacca ccagactgtt tcgcgtgttt accttcaaca tcggttaactt 360
 tctggcggat agtttcacgg taagcaacct gcggtttacc tacgttcgct tcaacgttga 420
 attcacgctt catacgggtca acgatgatgt cgaggtgcag ttccgccata cccgcgatga 480
 tggctctggtt agattcttcg tcagtccata cacggaaaga cgggtcttct ttagccagac 540
 gggccanagc cagaccatt ttttcctggt cagctttggt tttcgggtcaa ctgcgatgga 600
 gattaccggc tcanggaatt tccatacctt ccaggaatga tcggcgcatt ccggtcaaac 660
 angngtacc aggggggtac ntntttttaa nancgattgc cagcancgga tntnncccg 720
 gccnaacttc tttggaacnn tttaccggtt ggtaaccngc cttttnaacn atccaaccga 780
 aaaagngtta anngccantt ttcnngngt tnanntncgg nttcccngaa ntaaccnc 840
 cggggtnaac ccngnaaaa 859

<210> 23
 <211> 269
 <212> DNA
 <213> E. Coli

<400> 23
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 agtcaacgtc atggtaagaa ccgaagtga gacgaatacc catgtctact accgggtagc 120
 ctgccagcgg acctgctttc agctgttcct ggataccttt atcaacggcc gggatgtatt 180
 cgccagggat tacaccacct ttaatgtcgt tgatgaactc gtagcctttc gggtttgaac 240
 ccggctccag cgggtacatg tcgataaca 269

<210> 24
 <211> 330
 <212> DNA

<213> E. Coli

<400> 24

gttttgggga	gatgtaagg	ctaactctgaa	tggtctgcatt	ccttggtttaa	ggaaaaacga	60
atgactgatt	gccgatacct	gattaaacgg	gtcatcaaaa	tcatcattgc	tgttttacag	120
ctgatccttc	tggtcttata	acacaaggaa	acgtacttaa	ggtgcgtccg	gtgaaccagt	180
cggacgcacc	tttaataact	ataaataagt	gtctgggcag	atactatata	aattaactta	240
gtgaatgatt	atgctaattg	catcaattaa	ataaatataa	tggtcgtaag	gcttcccagt	300
aatataatta	atactctact	tccagagtag				330

<210> 25

<211> 471

<212> DNA

<213> E. Coli

<220>

<221> misc_feature

<222> (1)...(471)

<223> n = A,T,C or G

<400> 25

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atgactgatt	gccgatacct	gattaaacgg	gtcatcaaaa	tcatcattgc	tgttttacag	120
ctgatccttc	tggtcttata	acacaaggaa	acgtacttaa	ggtgccgtcc	ggtgaaccag	180
tcggacgcac	ctttaataac	tataaataag	tgtctgggca	gatactatat	aaattaactt	240
agtgaatgat	tatgctaattg	tcatcaatta	aataaatata	atggcgtaaa	ggcttcccag	300
taatataatt	aatactctac	ttccagagta	gaatattaaa	ttttatccgc	gtggtgcac	360
agcaciaaatt	tatcccacaa	ctgttcttct	gtctcgacat	gccccccgat	ctttnacaaa	420
tantattggg	ggattnggcc	cncctttttg	ncaggttggg	gtcctctnat	g	471

<210> 26

<211> 379

<212> DNA

<213> E. Coli

<220>

<221> misc_feature

<222> (1)...(379)

<223> n = A,T,C or G

<400> 26

natctgantg	gctgcattcc	ttgtttaagg	aaacccgaat	gactgattgc	cgatacctga	60
ttaaacgggt	catcaaaatc	atcattgctg	ttttacagct	gatccttctg	ttcttataac	120
acaaggaaac	gtacttaagg	tgcggtccgg	gaaccagtcg	gacgcacctt	taataactat	180
aaataagtgt	ctgggcagat	actatataaa	ttaacttagt	gaatgattat	gctaattgtca	240
tcaattaaat	aaatataatg	gcgttaaggc	ttcccagtaa	tataattaat	actctacttc	300
cagagtagaa	tattaaattt	tatccgcgtg	gtgcatcagc	acaaatttat	cccacaactg	360
ttcttctgtc	tcgacatgc					379

<210> 27

<211> 799

<212> DNA

<213> E. Coli

<400> 27

aaagatgatg	tgatgagaaa	gtcaatttga	ataagacaat	attaagagct	aaaaaaatgt	60
caaaaaacac	taaatcaaaa	aataatggca	ttagaaaata	taatgcgaaa	acggaggtga	120

aattagttta	tttcaaatga	ggaaaatctc	ccggcgaaaa	aaccgggaga	tgaaagtgtg	180
atgggtatca	aataaacaac	agaggagaaa	tttttaacgc	agccattcag	gcaaatacgtt	240
taatccatt	gcctggcgga	taagttgcgg	cttaacgcc	ggaagcgtgt	cggccagttt	300
caaaccaata	tcacgcagca	gttttttcgc	cggattggta	ccggaaaaca	gatcgcgga	360
tccctgcata	ccagccagca	tcaacgccgc	actgtgcttg	cggctacgct	catagcgacg	420
cagataaatg	tactgcccga	tgtctgggat	ccgtcgacct	gcagccaagc	ttgggctttt	480
cagcctgata	cagattaaat	cagaacgcag	aagcggctctg	ataaaacaga	atttgcctgg	540
cggcagtagc	gcggtggtcc	cacctgacct	catgccgaac	tcagaagtga	aacgcccgta	600
gcgcccgatg	gtagtgtggg	gtctcccat	gcgagagtag	ggaactgcca	ggcatcaaat	660
aaaacgaaag	gtcagtcga	aagactgggc	ctttcggttt	atctggtggt	tgtcgggtgaa	720
cgctctctga	gtaggacaaa	tccgccggga	gcggattttg	aacgttgcca	aacaaccggc	780
ccggaaagg	gtgggggct					799

<210> 28
 <211> 636
 <212> DNA
 <213> E. Coli

 <220>
 <221> misc_feature
 <222> (1)...(636)
 <223> n = A,T,C or G

<400> 28						
aggggggtttg	ttgtgggcaa	tgatgcattt	aagttatcgt	ctgcagatag	aggagatatt	60
acaataaaca	acgaatcagg	gcatttgata	gtcaataaccg	caattctatc	aggagatata	120
gtcactctaa	gaggaggaga	aattaggttg	gtattatagc	ttgtgcgcgc	catgattggc	180
gcgcaattta	aacttagtgc	tttacatcgc	tattgtcttg	atttctttga	attattttat	240
aaattaaaaa	aacgactggt	atgtataagc	aaaggtcgaa	cgaaaaatac	attccaaata	300
aatgcttgct	taaatctcta	tatccttccc	cgaaaaatga	cacataaaat	tgagatattc	360
caaaaagaga	tactacaaat	aaagatgcct	ttattttatt	atttctaata	aaaatagaag	420
caataaaaaa	taataacaat	gatataaatc	taatgttttt	aaatatattg	tcttttatgt	480
tagtaaatgt	cgtagtatg	tttgattctc	catatattac	gtgtagtttt	ttatatacat	540
ggaaataatt	ntctttatc	tgagacatca	caccatcatc	aaatggaagt	ttgaagatgg	600
tgcttggttt	gctaaccaat	aaaaagagtg	cattcgc			636

<210> 29
 <211> 757
 <212> DNA
 <213> E. Coli

 <220>
 <221> misc_feature
 <222> (1)...(757)
 <223> n = A,T,C or G

<400> 29						
cagcggctcgt	atttttagca	tggtttttta	ttggcggcta	tgctgccccg	ggagcataaa	60
gatgaaaaaa	acaacgatta	ttatgatggg	tgtggcgatt	attgtcgtac	tcggcactga	120
gctgggatgg	tggtaacgtc	acctctaaaa	aatagcaaag	gctgcctgtg	tcgagccttt	180
gtgcaattta	agcgttaact	tttaatcttc	ctgtagataa	atagcacgac	aatcgacca	240
ataacggcaa	ccacgaagct	gccaaaattg	aagccatcga	ctttaccaa	gccaaacagc	300
gtgctgatcc	atccgccgac	tacggcaccg	actatcccca	gcaggatagt	cataaagaat	360
ccacctccat	ctttacctgg	catgatccac	ttcgccagaa	taccggcaat	aagcccaaaa	420
ataatccatg	acagaatgcc	cattgtttcc	tcacttatct	gttttgcat	agcgggttag	480
tcgctgataa	aaagcatagc	acaacatcgc	gagggcaaga	tttgtgacga	gcatcacgga	540
ggtttttttt	gcgatggcgc	agaaattgcg	ccatcaacga	tcagtgataa	ttaccaacca	600

caaacatcat	gttcgttttc	cgtgtcataa	gaaccgtacg	ggattcacca	gatcttttat	660
cacttcaagc	cggcacttct	ggcaccagca	aagtcacg	cgtctctggg	tcataatcga	720
ccggaacgc	cattgctggg	attggtgacn	gtcacgg			757

<210> 30
 <211> 392
 <212> DNA
 <213> E. Coli

<400> 30						
aattacagaa	aaaggaggca	ataticgggta	aaggcattag	cccgcacgaat	acgtcgggct	60
acaaatatta	ttgtgctgca	ggtgttttag	cgggttggg	atccacagggt	tctaactgga	120
agaccacatc	gacctgatca	tcaaactgaa	tagcggcctg	ctcgtaagtt	tcctgggcgg	180
acaccggcgc	ggcatcggct	ttcatcatcc	gcaccattgg	gctgggctga	tagttggaaa	240
catggtagcg	cacgctatat	accggcccca	gtttacgatg	aaagccgttc	gccagttcct	300
gcgcctgatg	aatcgcggtta	tcaatcgctg	ccttacgcgc	tttgtcttta	taggcatccg	360
gctgcgccac	gcccagcgac	acagaacgaa	tt			392

<210> 31
 <211> 351
 <212> DNA
 <213> E. Coli

<400> 31						
ctatccttga	tgaaccgcg	agcaaagata	ggtgattacg	tcatgggttt	acagaaaatt	60
acagaaaaag	gaggcaatat	cgggtaaagg	cattagccc	acgaatacgt	cgggctacaa	120
atattattgt	gctgcagggt	tttagcggg	ttgttgatcc	acaggttcta	actggaagac	180
cacatcgacc	tgatcatcaa	actgaatagc	ggcctgctcg	taagtttcct	gggcggacac	240
cggcgcgga	tcggctttca	tcatccgcac	cattgggctg	ggctgatagt	tggaacatg	300
gtagcgcacg	ctatataccg	gccccagttt	acgatgaaag	ccgttcgcca	g	351

<210> 32
 <211> 762
 <212> DNA
 <213> E. Coli

<220>
 <221> misc_feature
 <222> (1)...(762)
 <223> n = A,T,C or G

<400> 32						
aattatgaaa	cactgtctgg	aatcgtctga	atgacgggca	catttgcgag	cacgcatcca	60
gtaataacac	aggaaactat	tttatctacg	cgttagcgat	agactgcttg	catggcgaaa	120
ggaggtaagc	cgacgatttc	agcgggacgc	tgaaacggga	aagcccctcc	cgagggaagg	180
gccataaata	aggaaagggt	catgatgaag	ctactcatca	tcgtggtgct	cttagtcata	240
agcttccccg	cttactaaga	ctaccagggc	gggggaaacc	ccgctctacc	ctcactcctg	300
aaagtatgcc	ttcacgataa	gattgtcaat	ccgcaggctt	tgtagtctgc	gatcctgcc	360
gcaaataattc	tttgcgagtc	gttacgcaat	aatcacagag	gaaactattt	tattcacgcg	420
ttagcgatag	actgcattca	gggcgaaagg	aggtaaagccg	atgatttcag	cgggacgctg	480
aaacgggaaa	gcctctccc	gagaagagg	cttttaataa	ggaaagggtt	atgatgaagc	540
acgtcatcat	actggtgata	ctcttagtga	ttagcttcca	ggcttactaa	gaacaccagg	600
gggaggggga	aacctcttc	taacctcac	ttctgaaatt	gggtgctatg	acgctggcgt	660
tactgcttan	cgctaccagt	ttgtctgccc	tggcggttgt	aacgccagat	cggtagccgt	720
ttggatattt	taatgaaagc	cgacaaatca	atcancgtga	cg		762

<210> 33

<211> 293
 <212> DNA
 <213> E. Coli

<400> 33
 gcacatttgc gagcacgcat ccagtaataa cacaggaaac tattttatct acgcgttagc 60
 gatagactgc ttgcatggcg aaaggaggta agccgacgat ttcagcgga cgctgaaacg 120
 ggaaagcccc tcccgaggaa gggggcataa ataaggaaag ggtcatgatg aagctactca 180
 tcatcggtg gctcttagtc ataagcttcc ccgcttacta agactaccag ggcgggggaa 240
 acccgcgtct accctcactc ctgaaagtat gccttcacga taagattgtc aat 293

<210> 34
 <211> 633
 <212> DNA
 <213> E. Coli

<220>
 <221> misc_feature
 <222> (1)...(633)
 <223> n = A,T,C or G

<400> 34
 atttacactt tttacgaaat catgggatca ctaacaaaat atcgcttgtc agttatattg 60
 tatggcagga aagatatgcg actgatatta cagatcccca aagtggagag tttatgacca 120
 ttaaaaaataa gatgttgctg ggtgcgcttt tgctggttac cagtgccgcc tgggccgcac 180
 cagccaccgc gggttcgacc aatacctcgg gaatttctaa gtatgagtta agtagtttca 240
 ttgctgactt taagcatttc aaaccagggg acaccgtacc agaaatgtac cgtaccgatg 300
 agtacaacat taagcagtgg cagttgcgta acctgcccgc gcctgatgcc gggacgcact 360
 ggacctatat ggggtggcgcg tacgtgttga tcagcgacac cgacggtaaa atcattaaag 420
 cctacgacgg tgagattttt tatcatcgct aaaaaaagcc ccctcatcat gagggggaaa 480
 tgcagacacc ttgntatttt ttattattag ccacttgctc gtcttgcttg gtattaagtc 540
 gtatttcacg ttgattaatg cnggtggctc cagtgcgcca gattaacttt gtttgatcg 600
 aagacgtagt aactggctgg ttatcggaat tgg 633

<210> 35
 <211> 569
 <212> DNA
 <213> E. Coli

<400> 35
 tatggcagga aagatatgcg actgatatta cagatcccca aagtggagag tttatgacca 60
 ttaaaaaataa gatgttgctg ggtgcgcttt tgctggttac cagtgccgcc tgggccgcac 120
 cagccaccgc gggttcgacc aatacctcgg gaatttctaa gtatgagtta agtagtttca 180
 ttgctgactt taagcatttc aaaccagggg acaccgtacc agaaatgtac cgtaccgatg 240
 agtacaacat taagcagtgg cagttgcgta acctgcccgc gcctgatgcc gggacgcact 300
 ggacctatat ggggtggcgcg tacgtgttga tcagcgacac cgacggtaaa atcattaaag 360
 cctacgacgg tgagattttt tatcatcgct aaaaaaagcc ccctcatcat gagggggaaa 420
 tgcagacacc ttgttatttt ttattattag ccacttgctc gtcttgcttg ttattagtcg 480
 tatttcacgt tgattaatgc ggttgctc agtgcgccag atttaacttt gtttgatcg 540
 tagacgtagt aactggctgg tatcggaat 569

<210> 36
 <211> 338
 <212> DNA
 <213> E. Coli

<400> 36

cgtattcaca	tccttttgat	tggtgataac	atgcgaatcg	gtattatttt	tccggttgta	60
atcttcatta	cagcggtcgt	atTTTTtagca	tggtttttta	ttggcggcta	tgctgccccg	120
ggagcataaa	gatgaaaaaa	acaacgatta	ttatgatggg	tgtggcgatt	attgtcgtac	180
tccggcactgc	ctgggatggg	ggtaacgtca	cctctaaaaa	atagcaaagg	ctgcctgtgt	240
gcagcctttg	tgcaatttaa	gcgttaactt	ttaatcttcc	tgtagataaa	tagcacgaca	300
atcgacacaa	taacggcaac	cacgaagctg	ccaaaatt			338

<210> 37
 <211> 375
 <212> DNA
 <213> E. Coli

<400> 37						
ctgaatattt	aaaaaggaaa	acgacatgaa	accgaagcac	agaatcaaca	ttctccaatc	60
ataaaatatt	tccgtggagc	atTTTTtattat	tgaatataga	ggtttaactc	cggtaaaaaa	120
caaagaagca	ttgaatgcag	ggaaaaataa	tatggccata	aaaaacatcg	aaagaaactc	180
ttttaattta	acatgtaaac	gcatggttaa	tcctcatatc	acgggtggag	tgtaagaac	240
atacataaat	ggagtcatgt	tttccctttt	ccatttatca	agttcctgtt	gccgttttag	300
tccatctcta	attgcatatt	ttaatttttc	tgataaatgg	cattgagcat	cgatttcatt	360
taaaacaact	gtaca					375

<210> 38
 <211> 446
 <212> DNA
 <213> E. Coli

<400> 38						
ttacgatagc	tattagtaaa	aataaagag	ttagctgtat	tgttatgtct	gtggcgaaat	60
tgactacett	cgTTTTtttg	attaagaatg	atTTTTtattat	cgtaagtaaa	attacatgaa	120
tatttaaaaa	ggaaaacgac	atgaaaccga	agcacagaat	caacattctc	caatcataaa	180
atatttccgt	ggagcatttt	attattgaat	atagaggttt	aactccggta	aaaaacaaag	240
aagcattgaa	tgagggaaa	aataatatgg	ccataaaaaa	catcgaaaga	aactctttta	300
atttaacatg	taaacgcatg	gttaatcctc	atatcacggg	tggagtgtta	agaacataca	360
taaatggagt	catgttttcc	cttttccatt	tatcaagttc	ctgttgccgt	tttagtccat	420
ctctaattgc	atattttta	ttttct				446

<210> 39
 <211> 392
 <212> DNA
 <213> E. Coli

<220>
 <221> misc_feature
 <222> (1)...(392)
 <223> n = A,T,C or G

<400> 39						
tcaccccggt	gccgattttc	aggcatcctg	atttaactta	gcacccgcaa	cttaactaca	60
ggaaaacaaa	gagataaatg	tctaatacctg	atgcaaatacg	agccgatttt	ttaatcttta	120
cggactttta	cccgcctggg	ttattaattg	cactgtnatc	cgggcgttcg	cccgccttaa	180
tcacaatagg	ctgtgtagcc	tgggcctggt	tctctttcac	ccgcgcgaga	gcggcagcaa	240
tcgcatcttt	atctttggct	gcagggttga	cggctgcgct	cttatgtcgt	tcaaggcgag	300
ccgctttttc	gcgctccaga	cgagcctggc	gcgcttcgaa	acgcgctttg	gcttctgcgg	360
cncgcttttc	ttcctgacga	atagccgcaa	tt			392

<210> 40
 <211> 208

<212> DNA
<213> E. Coli

<400> 40
taataacgct atctgcggat aaagcagaat aggtgggttaa cccagacat aaaccgagga 60
aaataatggt attgtatttc ataattctatt gtcccttagc gacagattgc tgtctgctgg 120
ttcagtaagg taccaggaga aacttcagga agcttggtact cgacaatata gtttgagttt 180
ttatctttgc cccatgaaac ctgtaatt 208

<210> 41
<211> 342
<212> DNA
<213> E. Coli

<400> 41
catcctcaat accgttaaat gcaacccgaa ccccggttgt ccccttgctg cattcactta 60
acgtaattctg aaaagggacg gctggacttg tgctaccggt cgttggaat tgtctggcac 120
tgtttttttg gagatctacg gtaaaattaa gcgaatccga tgagactgtg cagccataat 180
cgaggacgag cccgctaatt ttaataacgc tatctgcgga taaagcagaa taggtgggta 240
acccagaca taaaccgagg aaaataatgt tattgtattt cataatctat tggttccttag 300
cgacagattg ctgtctgctg gttcagtaag gtaccaggag aa 342

<210> 42
<211> 841
<212> DNA
<213> E. Coli

<220>
<221> misc_feature
<222> (1)...(841)
<223> n = A,T,C or G

<400> 42
agatttactg ccaatttccg gcagatcgga aagggttaaa ccatattgat ccataagggg 60
acgaatcacg gctataccgc caggcatggc ttgagccatg gcattaaatt ccgcaaattc 120
gggcgctgat tcttcccacg cgggtatttt ggcacacacc agatccagca aggggttntc 180
aggatcggtg agcagcagat gatctaccag ttncagcgcc tgggtgtatt gntccttggt 240
ctgaataccc gnnagaaaag gtgccacagc anttagcttn tctcctgctt gcaagatgtc 300
tggcaatngc aatcattttt tgcacttant acgatgnaca ncngtaaaga aatcgnattt 360
ttntatgccg tcataacttt acgtatgtan cactttttgc nattcnaaaa aagaccattn 420
gctncaacac gtaaattna ttgncccna catttanaac ataaatgntt aaaattttcc 480
ccccncnnan ttttaagntn ttanagaat ngggaattac ctgcttttna atgnactcan 540
anttttttng naataattcc tntatcnaan ctntttttcn cccaanagnc nnccaaattn 600
cggtttnntn nttnnnngg cnttttttta cccnanaann tttattcaan nccttttttg 660
tagntatatt naagnggntt ttnttnnatt aactttccnn ttggncaaatt tttggcnnat 720
tttatatan aattntctta tntcntaatt tnggnanccc cngatgnaan tttatggngg 780
gantcccnnt ccctntttta tnnatgntct gggntatttt taaancctnn attaanannan 840
c 841

<210> 43
<211> 215
<212> DNA
<213> E. Coli

<400> 43
aataactttt cgtaggcag ttttgggtgt gagttgcaag aggggagact actgaataac 60
tcaagtttta taatcgaggg gaaaatggtg atggcggtta tagcaaaacg ccctcaacca 120

taaaggtcga	gggcgcttaa	gatgttaaaa	acccgctatc	cgttaaaaaa	caatgttcaa	180
ctaaggtcag	tgacattgcg	ctaaaaaagc	gaatt			215

<210> 44
 <211> 395
 <212> DNA
 <213> E. Coli

<220>
 <221> misc_feature
 <222> (1)...(395)
 <223> n = A,T,C or G

<400> 44						
gcattattca	tgagaaatgt	gtatcgtaaa	tcaactgaaa	ttaacgcaac	catttgttat	60
ttaaggttta	attatctgtg	tgtgatattt	tattgaatgt	tttaaatatt	gtttttattg	120
gcattgctat	aatattgggt	atcatttgct	gaatggattc	agtcttaatg	agtgggtttt	180
taagggacag	gcatagagta	atgatacgta	tgcataacca	acatctttac	tcattatgtc	240
attgaatgtt	gaccctatgt	gtttatgaag	gagaggtatt	ttcagttgat	ctggattgnt	300
aaattcatat	aatgcgctt	tgctcatgaa	tggatgccag	tatgtagtgg	gaaattataa	360
atattgaaat	agtccaacta	cttctttatt	accaa			395

<210> 45
 <211> 883
 <212> DNA
 <213> E. Coli

<220>
 <221> misc_feature
 <222> (1)...(883)
 <223> n = A,T,C or G

<400> 45						
ataatcaggt	aagaaaaggt	gcgcggagat	taccgtgtgt	tgcgatatat	tttttagttt	60
cgctggtcaa	tacatcagtg	gcaataaaac	gacatatcca	gaaaaatata	cactaagtga	120
atgatattct	ccgatttatc	ttaatcgttt	atggataacg	gcaaagggct	tcgttttttc	180
ctatacttat	tcagcactca	caaataaagg	aacgccaatg	aaaattatac	tctgggctgt	240
attgattatt	ttcctgattg	ggctactggg	ggtgactggc	gtatttaaga	tgatatttta	300
aaattaatta	atgtcatcag	gtccgaaaat	aacgagaata	tttcagtctc	tcacccctgt	360
gcgctcctgt	catgtgcatt	gcttcatata	atcactggcg	caaggagcgc	cgcaggcgna	420
gnntgcncgn	cgncccacct	naccccatgc	cgaacttcag	aantgaaaac	nccntaacnc	480
cgatngtcgg	cgggngcctc	cccattgcnan	agtangggaa	ntgccangcg	ncnnattaaa	540
cgaaaggctn	attncaaaga	ctgggccttn	cntttatctg	atgtttgtcg	gagaacgctc	600
tcctgagnan	gacaaatncc	gccgggagcg	gatttgaacn	ttgcgaagca	accgnccna	660
agggngnngt	cntgacnccc	nnctctanct	nnngccttc	ttttgcttna	angncctcct	720
anengatggc	cttttngcc	ntctacaaa	cnntttggtt	aatgcttnta	aaancctttc	780
cannntncaa	tcngtnntn	cccattcnnn	tnntgaaagn	ntnccnccn	tgtncantnt	840
anntnngggg	gnngngngcc	ggcggncccc	ccccccccc	ccc		883

<210> 46
 <211> 1024
 <212> DNA
 <213> E. Coli

<220>
 <221> misc_feature
 <222> (1)...(1024)

<223> n = A,T,C or G

<400> 46

gtttatggat	aacggcaaag	ggcttcgttt	tttcctatac	ttattcagca	ctcacaaata	60
aaggaacgcc	aatgaaaatt	atactctggg	ctgtattgat	tattttcctg	attgggctac	120
tgggtggtgac	tggcgtat	aagatgat	tttaaaatta	attaatgtca	tcagggtccga	180
aaataacgag	aatatttcag	tctctcatcc	tgttgcgctc	ctgtcatgtg	cattgcttca	240
tataatcact	ggcgcaagga	gcgcgcagag	tctccnant	nnnnntnntt	ntntnnctnn	300
nccttcacna	tncnnccn	nantnnatag	nncaccnntn	ttnttcnnnn	gnccnccctcc	360
nnncnnnnnn	ncatnnnatc	ccactnnntt	tntccannnn	nnncnnnnntn	cannccnaciaa	420
antncnaccn	anntnacctt	atacnnannc	nancnnnnnn	nnccactctn	netcgnnctc	480
ccccttcnac	nnccannnnn	cancnntcnn	ctnnnnccct	nnctaattn	ttctnnctan	540
ntcctanccn	cnnacnnncc	cancnatccn	nnnatacant	cnattnnntn	cnntcncntn	600
cncnnttcc	nnctnnnnc	tncncatnc	ccnnnannan	cannntcccc	ncctnccctna	660
ccnncnncnc	ccnccatccc	nnnccnncnt	ccnnantnga	caannnnaat	cncnnnnncn	720
nnnnnnnnnn	tnnnncccn	gcnncnccnt	ncntcacnc	tnnnnnncta	nannnnntac	780
nntnaccnnt	cctnncaacn	tnccctnnng	antccnacna	ntnnnnnnanc	nanaacnctn	840
tnnnnccata	atcccacacc	acnccctnc	anctntntnt	ncntcntccc	ttcntatcnc	900
agctnnnnnt	netntnnnnn	tnccncccn	cnnactncnn	nnaccnncnn	cccantcagt	960
ccacntccn	cnnnnnnntn	nnnnnancan	ctnncaacnc	cnantaacct	nntnncacct	1020
tccc						1024

<210> 47

<211> 236

<212> DNA

<213> E. Coli

<400> 47

atatacacta	agtgaatgat	atcttccgat	ttatcttaat	cgtttatgga	taacggcaaa	60
gggcttcggt	ttttcctata	cttattcagc	actcaciaat	aaaggaacgc	caatgaaaat	120
tatactctgg	gctgtattga	ttattttcct	gattgggcta	ctgggtggtga	ctggcgtatt	180
taagatgata	ttttaaaatt	aattaatgtc	atcagggtccg	aaaataacga	gaatat	236

<210> 48

<211> 418

<212> DNA

<213> E. Coli

<220>

<221> misc_feature

<222> (1)...(418)

<223> n = A,T,C or G

<400> 48

cggagattac	cggtgtgtgc	gatataat	ttagtttcgc	gtggcaatac	atcagtggca	60
ataaaacgac	atatccagaa	aatatacac	taagtgaatg	atatcttccg	attnatctta	120
ntcgtttatg	gataacggca	aagggttcg	ttttttccta	tacttattca	gcactcaciaa	180
ataaaggaac	gccaatgaaa	attatactct	gggctgtatt	gattattttc	ctgattgggc	240
tactggtggt	gactggcgta	tttaagatga	tatttttaaaa	ttaattaatg	tcatcaggtc	300
cgaaaataac	gagaatattt	cagtcctca	tcctgttgcg	ctcctgtcat	gtgcattgct	360
tcatataatc	actggcgcaa	ggagcgcgca	nggggcggcc	aatcgccgcc	ggccctcg	418

<210> 49

<211> 550

<212> DNA

<213> E. Coli

<400> 49
ctgctagtta cagggaaacac taatgacaga cagctaaaag ccctgtttta ttacgtatta 60
caaacagggg atgccagcg ttttcgtgca tttattggtg agatagcgga acgcgcacca 120
caagaaaagg agaaactgat gaccattgct gacagattac gtgaagaagg cgcaatgcag 180
ggcaaacacg aagaagccct gcgtattgct caggagatgc tggatagagg tttagacaga 240
gagttagtta tgatgggtgac ccgactttca ccagacgatc ttatcgcgca aagccactaa 300
tcctgtaaca ccgggagtta actggcggat gtttgctgta aaccacatca gcgaacgaca 360
tccgccagcg cctcttctaa atcgtaccag cgaaacgcaa aaccgccttc ttccagccgt 420
ttaggcagcg cgcgttgctc acctaatacc agtactgaag attcgcccat taacagtcga 480
atggcggtcg cggggacgcg caaaatggcc gggcgatgca gcgcatgacc gagcgcattg 540
gcaaattggt 550

<210> 50
<211> 99
<212> DNA
<213> E. Coli

<400> 50
ttggcatctc ggtgttgccg atcttcatga tatccagccc gccggaaact tcttcccaaa 60
cggttttgct gttatccatt gagtcacgga actgcccct 99

<210> 51
<211> 259
<212> DNA
<213> E. Coli

<220>
<221> misc_feature
<222> (1)...(259)
<223> n = A,T,C or G

<400> 51
ccgtgccgag atgatcctgt naccatcatc cgttgtgaag tagtgattca cgacttcaag 60
gcgcttttca aaagggtatt ttggctttga catattaggg gctattccat ttcacgncc 120
aacaataatg gtgcagtaca tactcnttgg aaatcaacac aggaggctgg gaatgccgca 180
gaaatataga ttactttctt taatagtgat ntgtttcacg cttttatttt tnaanaagt 240
tnggcttact tcccggggn 259

<210> 52
<211> 877
<212> DNA
<213> E. Coli

<220>
<221> misc_feature
<222> (1)...(877)
<223> n = A,T,C or G

<400> 52
cagcagagcg cggccttctt cgtcagattt cgcagtagtg gtaatggtaa tatccaaacc 60
acgaacgcgg tcgactttat cgtagtcgat ttctgggaag atgatctgct cacggacacc 120
catgctgtag ttaccacgac cgtcgaaaga cttagcggac aggccacgga agtcacggat 180
acgaggtaga gcaatagtga tcaggcgctc aaagaactcc cacatgcgtt cgccacgcag 240
agttacttta cagccgatcg gatagccctg acggattttg aagcctgcaa cagatttgcg 300
tgctttggtg atcagcgggt tttgaccgga gattgctgcc aggtctgctg ctgcgttatc 360
cagcagtttt ttgtcagcga tcgcttcacc aacacccatg ttcagggtga tcttctcgac 420
ccgagggact tgcatgacag aattgtagtt aaactcagtc atgagttttt taactacttc 480

gtctttgtag	taatcatgca	gtttcgccat	cgtactactc	catgtcgggtg	aacgctctcc	540
tgagtaggac	aaatccgccg	ggagcggatt	tgaacgttgc	gaagcaacgg	cccggagggt	600
ggcgggcagg	acgcccgcga	taaactgcc	ggcatcaa	taagcagaag	gccatcctga	660
cggatggcct	ttttgcgttt	ctacaaactc	ttttggttat	ttttctaaat	cattcaaata	720
tgtatccgnt	catcccatcc	tatcgatgat	aagctgtcaa	acatgagaat	ttaatcaatc	780
taaagtttta	tggngttaa	cttgggctgg	cagnttncca	atggcttaat	cagtngaggg	840
ccctatntta	acgaactngg	ctantttngg	tcaatcn			877

<210> 53
 <211> 291
 <212> DNA
 <213> E. Coli

<400> 53

tgaacagcag	agatagcgcc	agtgcggcca	atgttttttg	tcctttaaac	ataacagagt	60
cctttaagga	tatagaatag	gggtatagct	acgccagaat	atcgtatttg	attattgcta	120
gttttttagtt	ttgcttaaaa	atattgttag	ttttattaaa	tgcaaaacta	aattattggt	180
atcatgaatt	tgttgatga	tgaataaaat	ataggggggt	atagatagac	gtcattttca	240
tagggttata	aatgcgacta	ccatgaagtt	tttaattgaa	agtattgggt	t	291

<210> 54
 <211> 282
 <212> DNA
 <213> E. Coli

<400> 54

ttattaaatg	caaaactaaa	ttattggtat	catgaatttg	ttgtatgatg	aataaaatat	60
aggggggtat	agatagacgt	cattttcata	gggttataaa	tgcgactacc	atgaagtttt	120
taattgaaag	tattgggttg	ctgataattt	gagctgttct	attcttttta	aatatctata	180
taggtctgtt	aatggatttt	attttttaca	ttttttgtgt	ttaggcatat	aaaaatcaac	240
ccgccatatg	aacggcgggt	taaaatattt	acaacttagc	aa		282

<210> 55
 <211> 293
 <212> DNA
 <213> E. Coli

<220>

<221> misc_feature
 <222> (1)...(293)
 <223> n = A,T,C or G

<400> 55

cgggggtccg	cgctcatcaa	caatcggggg	gcagcaagg	gctgaaacgg	gaaagcccct	60
cccgaagaag	ggccttgta	taaggaaagg	gttatgatga	agctcgtcat	catactgggt	120
gtgtngttac	tgtaagttt	cccgacttac	taacaactca	tcagaggggg	gagaaatcct	180
cccttaccct	tgttccttta	ctctaggttg	aaaaaacaac	agcgtcaata	ggcctgccat	240
gtacgaagcg	agatctgtga	accgctttcc	ggttagcctt	ttttatcctg	ttg	293

<210> 56
 <211> 300
 <212> DNA
 <213> E. Coli

<400> 56

tctgcgttcc	gctaaaagg	gcaaagtctc	aggacgttgc	agcgttttgc	gtgaccgctc	60
ggggaaggca	aaattgcctc	tgggaaagca	ttgcgcgggg	tccggcgctc	atcaacaatc	120

ggggggcagc	aaggggctga	aacgggaaa	cccctcccga	agaaggggcc	ttgtataagg	180
aaagggttat	gatgaagctc	gtcatcatac	tggttggtgt	gttactgtta	agtttcccga	240
cttactaaca	actcatcaga	ggggggagaa	atcctccctt	acccttggtc	ctttactcta	300

<210> 57
 <211> 359
 <212> DNA
 <213> E. Coli

<400> 57						
caacacagga	ggctgggaat	gccgcagaaa	tatagattac	tttctttaat	agtgatttgt	60
ttcacgcttt	tatttttcac	ctggatgata	agagattcac	tgtgtgaatt	gcatattaaa	120
caggagagtt	atgagctggc	ggcgttttta	gcctgcaaat	tgaaagagta	agagtcttcg	180
gcgggaaatt	attcccgcct	tacttacggc	gttgcgcat	ctcattgcac	ccaaatttat	240
tcttcacaaa	aataataata	gattttatta	cgcgatcgat	tatttatttc	ctgaaaacaa	300
ataaaaaaat	ccccgccaaa	tggcagggat	cttagattct	gtgcttttaa	gcagagatt	359

<210> 58
 <211> 700
 <212> DNA
 <213> E. Coli

<220>
 <221> misc_feature
 <222> (1)...(700)
 <223> n = A,T,C or G

<400> 58						
aaaccttttt	ctcctgtttt	tcatagaggg	caacccatgt	cctgacctgg	gttcggggga	60
cacaaaaacg	tgccgagatg	atcctgtaac	catcatcagt	tgtgaagtag	tgattcacga	120
cttcaaggcg	cttttcaaaa	gggtattttg	gctttgacat	attaggggct	attccatttc	180
atcgtccaac	aaaatgggtg	cagtacatac	tcgttggaat	tcaacacagg	aggctgggaa	240
tgccgcagaa	atatagatta	ctttctttaa	tagtgatttg	tttcacgctt	ttatttttca	300
cctggatgat	aagagattca	ctgtgtgaat	tgcatattaa	acaggagagt	tatgagctgg	360
cggcgttttt	agcctgcaaa	ttgaaaagat	aagagtcttc	ggcgggaaat	tattcccgcc	420
ttacttacgg	cgttgcgcat	tctcattgca	cccaaattta	ttcttcacaa	aaataataat	480
agattttatt	acgcgatcga	ttattttatt	cctgaaaaca	aataanaaaa	tccccgccaa	540
atggcaggga	tcttagattc	tgtgctttta	agcagagatt	acaggctggg	tacgttacca	600
gctgccgggc	ctttaacgcc	gctttcgatg	gtgaaggaca	ctttctgacc	ttcgtccaga	660
gattgtaacc	atcgggtctg	atagccnaga	aatgtccaac			700

<210> 59
 <211> 631
 <212> DNA
 <213> E. Coli

<220>
 <221> misc_feature
 <222> (1)...(631)
 <223> n = A,T,C or G

<400> 59						
tggtggcatt	gggtgctgga	gagagaaaac	ccccgcacgt	tgagggtatg	cacctgacaa	60
caccacgggg	gctaattctg	actctagacc	actcaagaat	agccgcgaaa	cgttgtcatt	120
acaacacagg	cggctatatg	acgttcgcag	agctgggcat	ggccttctgg	catgatttag	180
cggctccggg	cattgctggc	attcttgcca	gtatgatcgt	gaactggctg	aacaagcgga	240
agtaacgtgt	catgcggggc	tcaggctgcc	gtaatggcaa	tttgcgcccg	gaccaggccg	300

caggggggaa	actctgcggc	cttttttcgtt	cttactgcgg	gtaaggcacc	cagtcgccgc	360
cgttcaggcg	aacgtacggt	ttatcctggg	attgaataac	tactgcattt	gagttctcgg	420
agaccggtgc	tgttttgtggc	aaccactggg	tgagtttttt	ccagtcaaca	ttgtcttcgg	480
tgaaaatctt	gccatcgaga	acgcgaacca	ccagatcgga	gatagccagg	aagctgctcg	540
gttgttcgat	gacaatcggt	gccccctgat	gcggtgcctt	catgccgaag	aatttcaccc	600
caacggggac	gtcngtgata	gaccgggcta	g			631

<210> 60
 <211> 648
 <212> DNA
 <213> E. Coli

<220>
 <221> misc_feature
 <222> (1)...(648)
 <223> n = A,T,C or G

<400> 60

ggctcaggcn	tgctgattgt	ttttttgtgc	aatggcccn	tattagcgtc	gttgctgtcg	60
atggagagaa	tcataaacgt	ggtgaatgat	gattgttagc	aaggaaaact	gtcaaaaatc	120
ttcaaaaaat	ttgagggata	aggccggaat	ggctccggcc	agagggaagt	taaccgcgaa	180
gctgttgctg	cttgagggtc	gttttaacca	gacgccaggc	gctccatacg	ccaaaaccgc	240
gtctggccca	gcggaccagc	atattaggat	ggcgaatcgt	ccagatcgcc	atcacgctac	300
tgccaaccag	cgcccaggag	cgcgactta	gcagcatatt	ccancgacga	tcgtaagcgc	360
ctgttgcttc	cagccattca	cgacgactgg	cggaagggnc	cgcgntgac	caacttgnt	420
tttagntgta	tncanattan	attnataaac	gcagnanncn	ggtntgatta	atcntatttn	480
gctctngtct	ggtagtttagc	nncggnnngt	ctcntnttna	cccnnttcnn	tttannttac	540
natnngtaan	ttatntttnt	nngtctnant	tntanttgng	tactntaagt	ntatncgnnn	600
atnntnnnan	nnnncagnnc	ntntttttta	aatnntttnt	nanncnnc		648

<210> 61
 <211> 737
 <212> DNA
 <213> E. Coli

<220>
 <221> misc_feature
 <222> (1)...(737)
 <223> n = A,T,C or G

<400> 61

tgctaataatc	tttctcattg	agatgaaaat	taaggtaagc	gaggaaacac	accacaccat	60
aaacggaggc	aaataatgct	gggtaatatg	aatgttttta	tggccgtact	gggaataatt	120
ttattttctg	gttttctggc	cgcgattttc	agccacaaat	gggatgacta	atgaacggag	180
ataatccctc	acctaaccgg	ccccttggtta	cagttgtgta	caaggggcct	gattttttatg	240
acggcgaaaa	aaaaccgccca	gtaaaccggc	ggtgaatgct	tgcatggata	gattttgtgtt	300
ttgctttttac	gctaacaggc	attttctctgc	actgataacg	aatcgttgac	acagtagcat	360
cagttttctc	aatgaatggt	aaacggagct	taaactcggg	taatcacatt	ttgttcgtca	420
ataaacatgc	agcgatttct	tccggtttgc	ttacctcat	acattgcccg	gtccgctctt	480
ccaatgacca	catccagagg	ctcttcagga	aatgcgcgac	tcacacctgc	tgtcacggta	540
atgttgatat	gcccttcaga	atgtgtgatg	gcatggttat	cgactaactg	gcaaattctg	600
acaccgtcac	gacatgcttc	ttcatcatta	gccgctttga	caataatgat	aaattcttcg	660
ccccgtagc	gataaacctg	ttcgtaatna	cgcgccaac	tgggntaagt	aaagttgccca	720
gggtgccgta	atcttac					737

<210> 62
 <211> 648

<212> DNA
 <213> E. Coli

 <220>
 <221> misc_feature
 <222> (1)...(648)
 <223> n = A,T,C or G

<400> 62
 tgcttttgaa tatgtgctcg caatcttgag aaggaaatgg cgaccacgaa agaaaaggca 60
 aaaaccgata atctgaaaga acccaagtat ttcagtataa gcattgaatg ccgaccagta 120
 aactctttcg gattcaccga gaaagtgaan ccaaaatgat aatcgtatac ataagtcttt 180
 cgagtggctc gtttagcaaaa agtttcaaca atggagtaaa tacatccaac atatcaataa 240
 ctctcaactg taaggggatt gaaatggtaa cccagctct tgccttgagg ggtatagccg 300
 agaccaccga agccccggag gtggtgaaat aaaaccgggc acaacacgaa agggcgcat 360
 tccgatatcc ataaaagaag tcgggtcttt gtctggtaaa attaaattgg tgggaagtgc 420
 gcctccgggt tgtaaatacc gactttgctg ggtgtagcct ggcgcatca agtttttttc 480
 tgggaagtgc ctgatgtccg ccttttttaa agggaatttt ggtgatgccg gtgaatgccg 540
 cttaaccccc cgtgggccca gttaaaagtc atggtaagnc ctaatnggtt tgggggtggga 600
 aaagccnact gnnaattgggt tacctggttt gcaagtancc ctggaagg 648

<210> 63
 <211> 237
 <212> DNA
 <213> E. Coli

 <220>
 <221> misc_feature
 <222> (1)...(237)
 <223> n = A,T,C or G

<400> 63
 ggtgtttant tacaagagat tcatctttgt ntaaancccn gataagtaat tacgcataaa 60
 acaacaatga ttataatagc aaaaataaat attatcatct ttgatagatt acttgagata 120
 gccagcatct tgtaaagcct ttatcgTTTT tttatgctct ggattaatat aatcactaca 180
 tctatctgag caatctgttg ttgatggaca tgtcaaccga tggtcattta cagccaa 237

<210> 64
 <211> 427
 <212> DNA
 <213> E. Coli

<400> 64
 gataattaga gtttgtcgtc agaaaattga cgttacccat aacaaatgaa aggccaggta 60
 aatcatgccca ttagtcattg ttgctatcgg tgtaatcttg ttgttgctcc tgatgatccg 120
 cttcaaaaatg aacggcttca tcgctctcgt cctcgtggcg cttgctgttg gattaatgca 180
 aggaatgccg ctggataaag ttattggctc catcaaagcc ggtgtcggcg ggacgctcgg 240
 tagccttgcc ctgatcatgg gttttggcgc aatgctggcg aaaatgctgg cagactgcgg 300
 tggcgcacaa cgtatcgcca ccacgctgat tgccaaattt ggtaaaaaac acatccagt 360
 ggcgggtgga ctgaccgggt ttaccgttgg ttttgccctg ttctatgaag tgggctttgt 420
 gctgatg 427

<210> 65
 <211> 261
 <212> DNA
 <213> E. Coli

<220>
 <221> misc_feature
 <222> (1)...(261)
 <223> n = A,T,C or G

<400> 65

caaagaacct tcaacatgaa aaatatccat ttgtttgcaa aaaaagatta ttaggaagga	60
aattaatgca attatcgaaa attcaaaaaa tatccaaaaa tngtatactt tattccagaa	120
gagttcaata taatgtttgt cttcaatttt tcttacttca gggtaatata gattgctcat	180
tacattgtga gcttcacett tatttaattt tctgttgact ccagctctcc gtgataacgg	240
ttttataatt agatgcttat c	261

<210> 66
 <211> 98
 <212> DNA
 <213> E. Coli

<400> 66

agatgattgc cgggaacttg ttagcggcac gcaggcggcg gctcgcaccc ttaccctgct	60
ctttacgtac ttctgcgttg atagtaaaca tttctttc	98

<210> 67
 <211> 260
 <212> DNA
 <213> E. Coli

<400> 67

aagcgcgaac gaatcgatg tgctgcagct tcggtttgta cgggtgacgc tgtacgtcct	60
gagctttaac tttgatttct ttaccgtcaa caacgatggc cagaacttcg ctgtagaatt	120
cagcttttagc ttgcatgttc atgactttgt cgtgatccag ctcgatagcc agcggcgctt	180
ctttgccacc gtagatgatt gccgggaact tgttagcggc acgcaggcgg cggctcgcac	240
ccttaccctg ctctttacgt	260

<210> 68
 <211> 95
 <212> DNA
 <213> E. Coli

<400> 68

aaaaacggcg taaagaaagg ttgcaaacat gttaataaaa actcaaattg atcccacgta	60
tatattacgc cgcaaaatcc ttacaataaa caggg	95

<210> 69
 <211> 174
 <212> DNA
 <213> E. Coli

<400> 69

ttaattatta aaatagtgtg acgcgattat gtggttatgg gggtaaacat taaataaacc	60
agcggggagg ggaggtaaag tgaaaaaata aaaagcggat aatcttaata agcaggccgg	120
acagcatcgc catccggcac tgatacgagg tttatttcag ctcatcaacc atcg	174

<210> 70
 <211> 138
 <212> DNA
 <213> E. Coli

<400> 70
 agtctgtataa aacgtcaaaa agagtgtttt atcaacagaa gaatggaggt ctgacagata 60
 gtagtaatgc aaaaaaatgg agacttaagt tgaatgaacg ggagtaaagc gaaaagacta 120
 tagagtgaag gagaaatt 138

<210> 71
 <211> 191
 <212> DNA
 <213> E. Coli

<400> 71
 tttgttggct taatattcta ttgttatctt tatttataga tgtttatatt gcatgaggtg 60
 gtttttggag agaagaatga ggaagatgcg tgcagccaca gaaacgttag ctttacatat 120
 agcggaggtg atgtgaattt aatttacaat agaaataatt tacatatcaa acagtttagat 180
 gctttttgtc g 191

<210> 72
 <211> 244
 <212> DNA
 <213> E. Coli

<400> 72
 ggccatttat acaggaaaag cctatgtcag aacgtaaaaa ctcaaaatca cgccgtaatt 60
 atctcgttaa atgttcctgc ccaaactgca cccaagagtc agaacacagt ttttcaagag 120
 tacaaaaagg tgcccttttg atctgccctc attgcaacaa agtattccag acaaattcta 180
 aagctgtagc ctgattgatt ttattagtaa caagtatttt ttatatattta ataatatatt 240
 taaa 244

<210> 73
 <211> 327
 <212> DNA
 <213> E. Coli

<220>
 <221> misc_feature
 <222> (1)...(327)
 <223> n = A,T,C or G

<400> 73
 aaattttcag gtaccttgtc accatacttt tttttctgag cattaatgat attttgagct 60
 tcttgaggat ctttaactcc ccacatttgg tggaaagtat tcatattaaa aggaaggntg 120
 aataatttgn ctttataaat cgccagtgga gaattagtaa aacgattaaa ttctactaaa 180
 tnattaaccg naaaaaaatt cccatatata tttatcattg gtatgaaaaa tatgtgcacc 240
 atatttatga atntggatc cctnacagtc ctctgtgtac gcatttccac cgatatgatt 300
 tcttttctna atcactaaaa ctttttt 327

<210> 74
 <211> 150
 <212> DNA
 <213> E. Coli

<400> 74
 gcagtgatcg aagcgatgac gaagtgtatg gaaaaatcag aaaaactcag caaatcctga 60
 tgactttcgc cgacgtcag gccgccactt cggtgcggtt acgtccggct ttctttgctt 120
 tgtaaagcgc caaatctgcc gatttcaacc 150

<210> 75

<211> 330
 <212> DNA
 <213> E. Coli

<400> 75
 gaaagtatct tcgttattga catcactgga aaatataact tgcttttcat tattaaactc 60
 gaagcgcgta ccgtatctgg acaaacattt atcgagctta ccaaattcct gaagagggtt 120
 aactacagat aacatttgcg cgtcctttgc agtaatgccc gtcaaatacct tgacgggcat 180
 tatttagatt aaattaccag tatttcttcg gagtgaagaa tattaccagg tatatttaac 240
 acccaggttc gcggaccagt cttgatctac gtcaccacca ccgaggtagt tagcatcggt 300
 ataggcgctg aagttcttgg tgaagctaaa 330

<210> 76
 <211> 194
 <212> DNA
 <213> E. Coli

<400> 76
 tgtttttttc cagcaacgga gcaaaagggt tgcccttgtg cagctcaggg ttaaccactt 60
 taactacgtg gcgacgaccc ggagatgtcg gtttacattt aacaactgcc attgtattac 120
 tcctccgact tactcagcgc cgccaacgaa gtccagattc tggccttctt tcagggtgac 180
 gtaagctttt ttcc 194

<210> 77
 <211> 188
 <212> DNA
 <213> E. Coli

<400> 77
 tccctttaac taccagggtg ttaacgactt cgacttcgac ttcaaacagt ttctgcacag 60
 cagctttgat ttctgcttgg gtcgcgtctt tagcaacttt gactactatg gtgttggtg 120
 tttccatcgc agtagacgct ttttcagaaa cgtgcggtgc acgcagcacc ttcagcagac 180
 gttcttca 188

<210> 78
 <211> 173
 <212> DNA
 <213> E. Coli

<400> 78
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<210> 79
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 <213> E. Coli

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 <211> 259
 <212> DNA
 <213> E. Coli

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<210> 81
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 <213> E. Coli

<400> 81						
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 <211> 666
 <212> DNA
 <213> E. Coli

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 <211> 612
 <212> DNA
 <213> E. Coli

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<210> 84
 <211> 975
 <212> DNA
 <213> E. Coli

<400> 84						
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 <211> 1761
 <212> DNA
 <213> E. Coli

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<210> 86

<211> 1185

<212> DNA

<213> E. Coli

<400> 86

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<210> 87

<211> 2115

<212> DNA

<213> E. Coli

<400> 87

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 <211> 540
 <212> DNA
 <213> E. Coli

<400> 88						
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 <213> E. Coli

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<210> 90
 <211> 375
 <212> DNA
 <213> E. Coli

<400> 90						
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<210> 91
 <211> 366
 <212> DNA
 <213> E. Coli

<400> 91						
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<210> 93
 <211> 2145
 <212> DNA
 <213> E. Coli

<400> 93

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<210> 94
 <211> 1767
 <212> DNA
 <213> E. Coli

<400> 94

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<400> 96

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<210> 97

<211> 771

<212> DNA

<213> E. Coli

<400> 97

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<210> 98

<211> 1335

<212> DNA

<213> E. Coli

<400> 98

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<210> 99

<211> 1536

<212> DNA

<213> E. Coli

<400> 99

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<210> 100

<211> 1029

<212> DNA

<213> E. Coli

<400> 100

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<210> 101

<211> 993

<212> DNA

<213> E. Coli

<400> 101

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<210> 102

<211> 1023

<212> DNA

<213> E. Coli

<400> 102

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<210> 103
 <211> 876
 <212> DNA
 <213> E. Coli

<400> 103

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<210> 104
 <211> 291
 <212> DNA
 <213> E. Coli

<400> 104

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<210> 105
 <211> 1152
 <212> DNA
 <213> E. Coli

<400> 105

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 <211> 3048
 <212> DNA
 <213> E. Coli

<400> 106

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<210> 107

<211> 885

<212> DNA

<213> E. Coli

<400> 107

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<210> 108

<211> 654

<212> DNA

<213> E. Coli

<400> 108

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<210> 109

<211> 261

<212> DNA

<213> E. Coli

<400> 109

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<210> 110
 <211> 1203
 <212> DNA
 <213> E. Coli

<400> 110						
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<210> 111
 <211> 1179
 <212> DNA
 <213> E. Coli

<400> 111						
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<210> 112
 <211> 1326
 <212> DNA
 <213> E. Coli

<400> 112

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<210> 113
 <211> 585
 <212> DNA
 <213> E. Coli

<400> 113

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<210> 114
 <211> 363
 <212> DNA
 <213> E. Coli

<400> 114

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<210> 115
 <211> 921
 <212> DNA
 <213> E. Coli

<400> 115

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 <213> E. Coli

<400> 116

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 <213> E. Coli

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 aaaagttaa 249

<210> 118
 <211> 183
 <212> DNA
 <213> E. Coli

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 <211> 360
 <212> DNA
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 <211> 741
 <212> DNA
 <213> E. Coli

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 <212> DNA
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<400> 121

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 <211> 3123
 <212> DNA
 <213> E. Coli

<400> 122

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<211> 3078

<212> DNA

<213> E. Coli

<400> 123

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<211> 1416

<212> DNA

<213> E. Coli

<400> 124

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<210> 125

<211> 1035

<212> DNA

<213> E. Coli

<400> 125

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<210> 126

<211> 2481

<212> DNA

<213> E. Coli

<400> 126

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<400> 132

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cagcaacagg	ctaattgcgt	accagaagaa	caggttgatc	cgcgcaaagc	ggcagttgcc	2160
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<210> 133

<211> 1059

<212> DNA

<213> E. Coli

<400> 133

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gtactcaaac	tacgcaagca	gtcggtagcc	gcaacgttga	aagataactc	agcattgctg	240
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cctgacggcg	tggcttttgc	cgtcctgctg	gcgaacatca	cggttcctct	gatcgattac	1020
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<210> 134
 <211> 621
 <212> DNA
 <213> E. Coli

<400> 134						
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caacaaaagg	cgttatttga	tcaggtgctg	ccagccgaac	gctataacaa	tgcgctggca	180
cagagttgct	atctggtaac	tgcgccagag	ttaggtaaag	gtgagcatcg	ggtttacatc	240
gccaaacagg	atgacaaacc	ggtagccgcc	gttctggaag	caaccgcgcc	agatggctat	300
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tggatcacc	atgttgcggg	taaaaaaatc	agtgggtgag	atgatgcgca	ctgggcgggtg	480
aagaaagatg	gtgggtgattt	cgaccagttc	accggcgcgga	cgattactcc	ccgcgcgggtg	540
gttaatgcgg	taaaacgcgc	cggattgtac	gctcagacgt	taccggcaca	actttctcaa	600
cttcctgcct	gtggagaata	a				621

<210> 135
 <211> 696
 <212> DNA
 <213> E. Coli

<400> 135						
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cagttgctcg	gcctttgtcc	tctgttggcg	gtcacgtcca	ctgccactaa	cgctctgggt	120
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gccatgttcg	tgctgggttc	actacgcgaa	attatcgga	atggcacatt	gtttgacggt	480
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gcaggaaaaat	acctgattga	tgaaagaatg	aaaaagcgcc	gtgctgaagc	agctgcagaa	660
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<210> 136
 <211> 636
 <212> DNA
 <213> E. Coli

<400> 136						
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ctgcacgggc	gttatacctg	cattgcccgc	aagccccgct	gtggctcttg	tattattgaa	600
gatctttgtg	aatacaaaga	gaaagttgac	atctga			636

<210> 137
 <211> 504
 <212> DNA
 <213> E. Coli

<400> 137

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aatgtgatct	acacctggca	ataa				504

<210> 138
 <211> 531
 <212> DNA
 <213> E. Coli

<400> 138

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ttatccgcag	atagcgttat	taaaattagc	gggcgcgtcc	tcgattatgg	ctgcacagtc	120
tcatcggtat	cgcttaattt	taccgtagat	ctccaaaaaa	acagtgccag	acaatttcca	180
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ccagaacaga	acaatattht	gccttactcc	gctcgtctga	agtcaactca	gaagtccgtc	480
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<210> 139
 <211> 1149
 <212> DNA
 <213> E. Coli

<400> 139

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cttggaat	acggtacgac	atttttcagt	gccagtcgcc	aaagttaactg	gaacacgtca	180
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<210> 140

<211> 417

<212> DNA

<213> E. Coli

<400> 140

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<210> 141

<211> 315

<212> DNA

<213> E. Coli

<400> 141

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ttaaaagcag	tattcccatc	tctggataac	ttcaaatac	tggataagca	ttatgttttc	180
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tacatacgtg	aagttatgac	gcataaagaa	tacgatttct	ttaccgctgt	tcatcgtact	300
aaggggaaaa	aatga					315

<210> 142

<211> 7152

<212> DNA

<213> E. Coli

<400> 142

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<210> 143

<211> 186

<212> DNA

<213> E. Coli

<400> 143

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<210> 144
 <211> 1197
 <212> DNA
 <213> E. Coli

<400> 144

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<210> 145
 <211> 291
 <212> DNA
 <213> E. Coli

<400> 145

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<210> 146
 <211> 948
 <212> DNA
 <213> E. Coli

<400> 146

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<210> 147

<211> 891

<212> DNA

<213> E. Coli

<400> 147

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<210> 148

<211> 1668

<212> DNA

<213> E. Coli

<400> 148

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cgcggttggtg	aactctccgg	tggtgagcgc	ggtcgtctgc	atctggcgaa	gctgctgcag	1380
gttggcgga	acatgctgct	gctcgacgaa	ccaaccaacg	acctggatat	cgaaaccctg	1440
cgcgcgctgg	aaaacgccct	gctggagttc	ccgggctgtg	cgatggttat	ctcgcacgac	1500
cgttggttcc	tcgaccgtat	cgccacgcac	attctggatt	accaggatga	aggtaaagtt	1560
gagttcttcg	aaggtaaactt	taccgagtac	gaagagtaca	agaaacgcac	gctgggcgca	1620
gacgcgctgg	agccgaagcg	tatcaagtac	aagcgtattg	cgaagtaa		1668

<210> 149
 <211> 522
 <212> DNA
 <213> E. Coli

<400> 149						
atgtcaaagc	caaaataccc	ttttgaaaag	cgcccttgaag	tcgtgaatca	ctacttcaca	60
actgatgatg	gttacaggat	catctcggca	cgtttttggtg	tccccgaac	ccaggtcagg	120
acatggggttg	ccctctatga	aaaacatgga	gaaaaaggtt	taattcccaa	acctaaaggc	180
gttagtgctg	atccagagtt	gcgtattaag	gtcgtgaaag	ctgtgatcga	gcagcacatg	240
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agaaacattg	caatatcagt	tgatccagaa	aaagcggcat	cagcattgga	gctgtcaaaa	420
gaccgacgca	ttgaggatct	tgaaaggcaa	gttcgatttc	ttgaaacgcg	gcttatgtat	480
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<210> 150
 <211> 852
 <212> DNA
 <213> E. Coli

<400> 150						
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gcggacgtta	aaaagcgtat	tagtgagatt	tatcacgaga	atagaggccg	atacggatac	180
cgtagggttaa	cgctgtctct	tcacgcagaa	gggaaacaga	ttaaccataa	agctgttcag	240
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agaggagagg	tagggcaaac	cgccccta	gttctccaaa	gagatttcaa	ggctacgcgg	360
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gagcatcctg	ttctgcactc	tgaccaggga	tggcagatc	gtatgagaag	atatcaaaat	600
atccttaaag	aacatgggat	taaacaaagc	atgtccagaa	aaggcaattg	tctggataat	660
gctgtgggtg	agtgtttctt	tggaaacctta	aagtcggagt	gtttttatct	tgatgagttc	720
agtaatatata	gcgaactgaa	ggatgctgtt	acggaatata	ttgaatacta	caacagcaga	780
agaattagcc	tgaaattaaa	aggtctgact	ccaattgaat	atcggaatca	gacctatatg	840
cctcgtgttt	aa					852

<210> 151
 <211> 117
 <212> DNA
 <213> E. Coli

<400> 151						
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gggtgcatcc	gtgtgatttg	cagtgccgag	ccgaagcata	aacagcgcca	aggctga	117

<210> 152

<211> 1332
 <212> DNA
 <213> E. Coli

<400> 152

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cgcagactgc	tgtttgttat	cgggtgcgctg	attgtgttcc	gtattggctc	ttttattccg	120
atccctggta	ttgatgccgc	tgtacttgcc	aaactgcttg	agcaacagcg	aggcaccatc	180
attgagatgt	ttaacatggt	ctctggtggt	gctctcagcc	gtgcttctat	ctttgctctg	240
gggatcatgc	cgtatatattc	ggcgtcgatc	attatccagc	tgctgacggg	ggttcaccca	300
acgttggcag	aaattaagaa	agaaggggag	tctggtcgtc	gtaagatcag	ccagtacacc	360
cgctacggta	ctctggtgct	ggcaatattc	cagtcgatcg	gtattgctac	cggtctgccg	420
aatatgcctg	gtatgcaagg	cctggtgatt	aaccggggct	ttgcattcta	cttcaccgct	480
gttgtaagtc	tggtcacagg	aaccatgttc	ctgatgtggt	tgggcgaaca	gattactgaa	540
cgaggtatcg	gcaacgggat	ttcaatcatt	atcttcgccg	gtattgtcgc	gggactcccg	600
ccagccattg	cccatactat	cgagcaagcg	cgtcaaggcg	acctgcactt	cctcgtgttg	660
ctgttggttg	cagtattagt	atttgcagtg	acgttctttg	ttgtatttgt	tgagcgtggg	720
caacgccgca	ttgtggtaaa	ctacgcgaaa	cgtcagcaag	gtcgtcgtgt	ctatgctgca	780
cagagcacac	atttaccgct	gaaagtgaat	atggcggggg	taatcccggc	aatcttcgct	840
tccagtatta	ttctgttccc	ggcgaccatc	gcgtcatggt	tcggggggcg	tactggttgg	900
aactggctga	caacaatttc	gctgtatttg	cagcctgggc	aaccgcttta	tgtgttactc	960
tatgcgtctg	caatcatctt	cttctgtttc	ttctacacgg	cgttgggttt	caaccgcgct	1020
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caaacggcga	agtatatcga	taaagtaatg	acccgcctga	ccctggttgg	tgcgctgtat	1140
attaccttta	tctgcctgat	cccggagttc	atgcgtgatg	caatgaaagt	accgttctac	1200
ttcgggtgga	cctcactgct	tatcgttggt	gtcgtgatta	tggactttat	ggctcaagtg	1260
caaactctga	tgatgtccag	tcagtatgag	tctgcattga	agaaggcgaa	cctgaaaggc	1320
tacggccgat	aa					1332

<210> 153
 <211> 435
 <212> DNA
 <213> E. Coli

<400> 153

atgcgtttta	atactctgtc	tccggccgaa	ggctccaaaa	aggcgggtaa	acgcctgggt	60
cgtggtatcg	gttctggcct	cggtaaaacc	ggtggtcgtg	gtcacaaagg	tcagaagtct	120
cgttctggcg	gtggcgtagc	tcgcggtttc	gaggggtggc	agatgcctct	gtaccgtcgt	180
ctgccgaaat	tcggcttcac	ttctcgtaaa	gcagcgatta	cagccgaaat	tcgtctgtct	240
gacctggcta	aagtagaagg	cggtgtagta	gacctgaaca	cgctgaaagc	ggctaacatt	300
atcggtatcc	agatcgagtt	cgcgaaagtg	atcctggctg	gcgaagtaac	gactccggta	360
actgttcgtg	gcctgcgtgt	tactaaaggc	gctcgtgctg	ctatcgaagc	tgctggcggt	420
aaaatcgagg	aataa					435

<210> 154
 <211> 180
 <212> DNA
 <213> E. Coli

<400> 154

atggcaaaga	ctattaaaa	tactcaaacc	cgcagtgcaa	tcggctcgtct	gccgaaacac	60
aaggcaacgc	tgcttggcct	gggtctgcgt	cgtattggct	acaccgtaga	gcgcgaggat	120
actcctgcta	ttcgcgggat	gatcaacgcg	gtttccttca	tgggttaaagt	tgaggagtaa	180

<210> 155
 <211> 504
 <212> DNA

<213> E. Coli

<400> 155

atgggtcaca	tcgaaaaaca	agctggcgaa	ctgcaggaaa	agctgatcgc	ggtaaaccgc	60
gtatctaaaa	ccgttaaagg	tggtcgtatt	ttctccttca	cagctctgac	tgtagttggc	120
gatggtaacg	gtcgcgttgg	ttttggttac	ggtaaagcgc	gtgaagttcc	agcagcgatc	180
cagaaagcga	tgaaaaaagc	ccgtcgcaat	atgattaacg	tcgcgctgaa	taacggcact	240
ctgcaacacc	ctgttaaagg	tgttcacacg	ggttctcgcg	tattcatgca	gccggcttcc	300
gaaggtaccg	gtatcatcgc	cgggtggtgca	atgcgcgccg	ttctggaagt	cgctgggggt	360
cataacgttc	tggtctaaagc	ctatgggttcc	accaaccgga	tcaacgtggg	tcgtgcaact	420
attgatggcc	tgaaaaatat	gaattctcca	gaaatggtcg	ctgccaagcg	tggtaaatcc	480
gttgaagaaa	ttctggggaa	ataa				504

<210> 156

<211> 354

<212> DNA

<213> E. Coli

<400> 156

atggataaga	aatctgctcg	tatccgtcgt	gcgacccgcg	cacgccgcaa	gctccaggag	60
ctgggcgcaa	ctcgcctggt	ggtacatcgt	accccgcgctc	acatttacgc	acaggtaatt	120
gcaccgaacg	gttctgaagt	tctggtagct	gcttctactg	tagaaaaagc	tatcgctgaa	180
caactgaagt	acaccggtaa	caaagacgcg	gctgcagctg	tgggtaaagc	tgctcgctgaa	240
cgcgctctgg	aaaaaggcat	caaagatgta	tcctttgacc	gttccggggt	ccaatatcat	300
ggtcgtgtcc	aggcactggc	agatgctgcc	cgtgaagctg	gccttcagtt	ctaa	354

<210> 157

<211> 534

<212> DNA

<213> E. Coli

<400> 157

atgtctcgtg	ttgctaaagc	accggctcgtt	gttcctgccg	gcgttgacgt	aaaaatcaac	60
ggtcagggtta	ttacgatcaa	aggtaaaaac	ggcgagctga	ctcgtactct	caacgatgct	120
gttgaagtta	aacatgcaga	taataccctg	accttcggctc	cgcgtgatgg	ttacgcagac	180
ggttgggcac	aggctggtac	cgcgcgtgcc	ctgctgaact	caatggttat	cgggtgttacc	240
gaaggcttca	ctaagaagct	gcagctggtt	ggtgtaggtt	accgtgcagc	ggtaaaggc	300
aatgtgatta	acctgtctct	gggtttctct	catcctgttg	accatcagct	gcctgcgggt	360
atcactgctg	aatgtccgac	tcagactgaa	atcgtgctga	aaggcgctga	taagcaggtg	420
atcgccagg	ttgcagcgga	tctgcgcgcc	taccgtcgtc	ctgagcctta	taaaggcaag	480
ggtgttcgtt	acgccgacga	agtcgtgcgt	accaaagagg	ctaagaagaa	gtaa	534

<210> 158

<211> 393

<212> DNA

<213> E. Coli

<400> 158

atgagcatgc	aagatccgat	cgcggatatg	ctgacccgta	tccgtaacgg	tcaggccgcg	60
aacaaagctg	cggtcaccat	gccttcctcc	aagctgaaag	tggaatcgc	caacgtgctg	120
aaggaagaag	gttttattga	agatttttaa	gttgaaggcg	acaccaagcc	tgaactggaa	180
cttactctga	agtatttcca	gggcaaagct	gtttagaata	gcattcagcg	tgtagccgcg	240
ccagggtctg	gcatttataa	acgtaaaagt	gagctgccga	aagttatggc	gggtctgggt	300
atcgagttg	tttctacctc	taaagggtgt	atgactgata	gtgcagcgcg	ccaggctggt	360
cttgggtggc	aaattatctg	ctacgtagcc	taa			393

<210> 159

<211> 306
 <212> DNA
 <213> E. Coli

<400> 159

atggcctaagc	aatcaatgaa	agcacgcgaa	gtaaaacgcg	tagcttttagc	tgataaatac	60
ttcgcgaaac	gcgctgaact	gaaagcgatc	atctctgatg	tgaacgcctc	cgacgaagat	120
cgtttgaacg	ctgtttctcaa	gctgcagact	ctgccgcgtg	attccagccc	gtctcgtcag	180
cgtaaccgct	gccgtcaaac	aggtcgtccg	catggtttcc	tgcggaagtt	cgggttgagc	240
cgtattaagg	tccgtgaagc	cgctatgcgc	ggtgaaatcc	cgggtctgaa	aaaggctagc	300
tggtaa						306

<210> 160
 <211> 540
 <212> DNA
 <213> E. Coli

<400> 160

atggcgaaac	tgcatgatta	ctacaaagac	gaagtagtta	aaaaactcat	gactgagttt	60
aactacaatt	ctgtcatgca	agtccctcgg	gtcgagaaga	tcaccctgaa	catgggtggt	120
ggtgaagcga	tcgctgacaa	aaaactgctg	gataacgcag	cagcagacct	ggcagcaatc	180
tccgggtcaaa	aaccgctgat	caccaaagca	cgcaaactctg	ttgcaggctt	caaaatccgt	240
cagggctatc	cgatcggctg	taaagtaact	ctgcgtggcg	aacgcattgtg	ggagttcttt	300
gagcgcctga	tcactattgc	tgtacctcgt	atccgtgact	tccgtggcct	gtccgctaag	360
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atcgactacg	ataaagtcga	ccgcgttcgt	ggtttggata	ttaccattac	cactactgcg	480
aaatctgacg	aagaaggccg	cgctctgctg	gctgcctttg	acttcccgtt	ccgcaagtaa	540

<210> 161
 <211> 315
 <212> DNA
 <213> E. Coli

<400> 161

atggcagcga	aaatccgtcg	tgatgacgaa	gttatcgtgt	taaccggtaa	agataaagggt	60
aaacgcggta	aagttaagaa	tgtcctgtct	tccggcaagg	tcattgttga	aggtatcaac	120
ctggttaaga	aacatcagaa	gccggttcgg	gccctgaacc	aaccgggtgg	catcgttgaa	180
aaagaagccg	ctattcaggt	ttccaacgta	gcaatcttca	atgcggcaac	cggcaaggct	240
gaccgtgtag	gcttttagatt	cgaagacggg	aaaaaagtcc	gtttcttcaa	gtctaacagc	300
gaaactatca	agtaa					315

<210> 162
 <211> 372
 <212> DNA
 <213> E. Coli

<400> 162

atgatccaag	aacagactat	gctgaacgtc	gccgacaact	ccggtgcacg	tcgcgtaatg	60
tgtatcaagg	ttctgggtgg	ctcgcaccgt	cgctacgcag	gcgtaggcga	catcatcaag	120
atcaccatca	aagaagcaat	tccgcgtggg	aaggtcaaaa	aaggtgatgt	gctgaaggcg	180
gtagtggtgc	gcaccaagaa	gggtgttcgt	cgcccgacg	gttctgtcat	tcgcttcgat	240
ggtaatgctt	gtgttcttct	gaacaacaac	agcgagcagc	ctatcggtac	gcgtattttt	300
gggccggtaa	ctcgtgagct	tcgtagtgag	aagttcatga	aaattatctc	tctggcacca	360
gaagtactct	aa					372

<210> 163
 <211> 567

<212> DNA
<213> E. Coli

<400> 163

atgttttaaag	gacaaaaaac	attggccgca	ctggccgtat	ctctgctgtt	cactgcacct	60
gtttatgctg	ctgatgaagg	ttctggcgaa	attcacttta	agggggaggt	tattgaagca	120
ccttgtagaa	ttcatccaga	agatattgat	aaaaacatag	atcttggaca	agtcacgaca	180
acccatataa	accgggagca	tcatagcaat	aaagtggccg	tcgacattcg	cttgatcaac	240
tgtgatctgc	ctgcttctga	caacggtagc	ggaatgccgg	tatccaaagt	tggcgtaacc	300
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gcaacctacg	tgctggatta	taaaataa				567

<210> 164
<211> 1284
<212> DNA
<213> E. Coli

<400> 164

atggctgata	caaaagcaaa	actcaccctc	aacggggata	cagctgttga	actggatgtg	60
ctgaaaggca	cgctgggtca	agatgttatt	gatatccgta	ctctcggttc	aaaagggtgtg	120
ttcacctttg	accagggtt	cacttcaacc	gcattcctgcg	aattctaaaat	tactttttatt	180
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ctgttccatg	ctttccgtcg	cgactcgcat	ccaatggcag	tcatgtgtgg	tattaccggc	420
gcgctggcgg	cgttctatca	cgactcgctg	gatgttaaca	atcctcgtca	ccgtgaaatt	480
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gaaacctgcc	atgaagtgc	gaaagagctg	ggcacgaagg	atgacctgct	ggaagtggct	1020
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aacgtcgatt	tctactctgg	tatcatcctg	aaagcgatgg	gtattccgtc	ttccatgttc	1140
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tttaaaagcg	atatcaagcg	ttaa				1284

<210> 165
<211> 1434
<212> DNA
<213> E. Coli

<400> 165

atgaaagtaa	cgctgccaga	gtttgaacgt	gcaggagtga	tggtggttgg	tgatgtgatg	60
ctggatcggt	actggtagcg	ccccaccagt	cgatctctgc	cggaagcgcc	ggtgcccggtg	120
gttaaagtga	ataccatcga	agaacgtccg	ggcggcgcgg	ctaactgtgg	gatgaatc	180
gcttctctcg	gtgctaattc	acgcctggtc	gggttgacgg	gcattgacga	tgacgcgcgc	240
gcgctgagta	aattctctggc	cgacgtcaac	gtcaaagtcg	acttcgtttc	tgtaccgacg	300
catccgacca	ttaccaaat	acgggtactt	ttccgcaacc	aacagctgat	ccgtctggat	360
tttgaagaag	gtttcgaagg	tggtgatccg	cagccgctgc	acgagcggat	taatcaggcg	420

ctgagttcga	ttggcgcgct	ggtgctttct	gactacgcc	aaggtgcgct	ggcaagcgta	480
cagcagatga	tccaactggc	gcgtaaagcg	ggtgttccgg	tgctgattga	tccaaaaggt	540
accgattttg	agcgctaccg	cggcgctacg	ctgttaacgc	cgaatctctc	ggaatttgaa	600
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gccgattacg	aactctcggc	tctgttagtg	acccgttccg	aacaggggat	gtcgcgtgctg	720
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gcaaattgcc	gcaagctggg	tgaccgcttg	attgttgccg	tcaacagcga	tgccctccacc	1140
aaacggctga	aaggggattc	ccgcccggta	aacccactcg	aacagcgtat	gattgtgctg	1200
ggcgcaactg	aagcggtcga	ctgggtagtg	tcgtttgaag	aggacacgcc	gcagcgcttg	1260
atcgccggga	tcttgccaga	tctgtgtgtg	aaaggcgcg	actataaacc	agaagagatt	1320
gccgggagta	aagaagctcg	ggccaacggt	ggcgaagtgt	tggtgctcaa	ctttgaagac	1380
ggttgctcga	cgaccaacat	catcaagaag	atccaacagg	ataaaaaagg	ctaa	1434

<210> 166

<211> 2841

<212> DNA

<213> E. Coli

<400> 166

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gagcctttag	ccgaggaatc	acttagcgca	caggcgaagt	cagtacttac	ttttagtgt	120
tttgtgcagg	acagcgtgat	tgcgcaccca	gagtggctga	cggaaactgga	aagccaaccg	180
ccgcaggccg	acgaatggca	gcattacgcg	gcatgggtgc	aggaggcgct	ctgtaatgtg	240
agtgcgaag	ccgggttaat	gcgcgagctg	cggctattcc	ggcggcgcat	tatggtgcgc	300
atcgccctgg	cgcaaacgct	ggcactggtt	actgaagaga	gcatattgca	gcagctcagc	360
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<210> 167

<211> 1302

<212> DNA

<213> E. Coli

<400> 167

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<210> 168

<211> 213

<212> DNA

<213> E. Coli

<400> 168

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ggttacaaat	ctctggacga	aggtcagaaa	gtgtccttca	ccatcgaaag	cggcgctaaa	180
ggcccggcag	ctggtaacgt	aaccagcctg	taa			213

<210> 169

<211> 1572
 <212> DNA
 <213> E. Coli

<400> 169

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cgctcatcat	ga					1572

<210> 170
 <211> 189
 <212> DNA
 <213> E. Coli

<400> 170

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<210> 171
 <211> 1680
 <212> DNA
 <213> E. Coli

<400> 171

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gccatttttg	ttttattagt	ggcctgggtta	ttcctgtcac	aatggattcg	cattaccggt	420

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<210> 172

<211> 384

<212> DNA

<213> E. Coli

<400> 172

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<210> 173

<211> 306

<212> DNA

<213> E. Coli

<400> 173

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<210> 174

<211> 405

<212> DNA

<213> E. Coli

<400> 174

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gaagaggaaa	aagcgaatct	ctttcaactt	ttactgatgc	tgggcctgac	gatgcttttc	180
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gcaaacgatc	ggcagctgct	cgaggaggag	tcccgtgagc	agtaa		405

<210> 175
 <211> 300
 <212> DNA
 <213> E. Coli

<400> 175						
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caacggctgg	atctttccgc	cagtcgtcgt	gaatggctgg	agacaacagg	cgcttacgat	120
cgtcgctgga	atatgctgct	aagtcctgcg	tcctggggcg	tggttggcag	tagcgtgatg	180
gcgatctgga	cgattcgcca	tcctaatatg	ctgggtccgt	gggccagacg	cggttttggc	240
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<210> 176
 <211> 483
 <212> DNA
 <213> E. Coli

<400> 176						
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taa						483

<210> 177
 <211> 891
 <212> DNA
 <213> E. Coli

<400> 177						
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<210> 178

<211> 612
 <212> DNA
 <213> E. Coli

<400> 178

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<210> 179
 <211> 177
 <212> DNA
 <213> E. Coli

<400> 179

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<210> 180
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 <212> DNA
 <213> E. Coli

<400> 180

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<211> 369

<212> DNA

<213> E. Coli

<400> 181

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gaaatatatg	ttaggtatcg	ctatggcgaa	cggattgcag	aagaagaaaa	accatattta	240
attacggaac	taccagatag	ttgggttggt	gagggagcaa	agttacctta	tgaagttgcg	300
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 <211> 711
 <212> DNA
 <213> E. Coli

<400> 182

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cagcagtatg	ataaggagtc	ggggctgtac	tacaaccgga	accggtacta	cgatccgttg	180
caggggcggg	atatcactca	ggacccgata	gggctggagg	ggggatggag	tctgtatgcg	240
tatccgctga	atccggtgaa	tggtattgat	ccattaggg	taagtcccg	agatgtagcg	300
ctaataagaa	gaaaagatca	actaaaccat	caaagagcat	gggatataat	atctgatact	360
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gggttgacat	gtccatcaac	aacagattgc	tcagatagat	gtagtgatta	tattaatcca	660
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<210> 183
 <211> 261
 <212> DNA
 <213> E. Coli

<400> 183

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aaacattaca	taaactatat	ggcaatacca	gaaaatgatg	gagtttttac	atggctccca	180
gatttttttc	cgcacgtagc	ggtggatata	tcaatataca	caaagttaga	agatgattat	240
ttttttctta	tttttcccta	a				261

<210> 184
 <211> 192
 <212> DNA
 <213> E. Coli

<400> 184

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ggtgaaatta	atgttacgca	ttattttata	acaaatattg	gagctggatt	gcctgatgct	180
tgtgcagagt	aa					192

<210> 185
 <211> 504
 <212> DNA
 <213> E. Coli

<400> 185

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aaactcaggc	cgcagtcggg	aacctcgcgc	atacagccgg	gcagtgcgct	catcgtctgc	120
gcggaaatgg	acgaacagtg	gggctatgtc	ggggctaaat	cgcgccagcg	ctggctgttt	180

tacgcgtatg	acagtctccg	gaagacgggt	gttgcgacg	tattcggtga	acgcactatg	240
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gatggctggc	cgctgtatga	atcccgctg	aagggaaagc	tgcacgtaat	cagcaagcga	360
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ctgaacataa	aacactatca	ataa				504

<210> 186

<211> 276

<212> DNA

<213> E. Coli

<400> 186

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ctgcagttca	cttacaccgc	ttctcaaccc	ggtacgcacc	agaaaatcat	tgatatggcc	180
atgaatggcg	ttggatgccg	ggcaacagcc	cgcattatgg	gcgttggcct	caacacgatt	240
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<210> 187

<211> 417

<212> DNA

<213> E. Coli

<400> 187

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agaaataatg	atgatttcat	aaaccctgat	ctacaagaac	ggttagtgat	cggggattat	360
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<210> 188

<211> 1179

<212> DNA

<213> E. Coli

<400> 188

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tatcctccca	tgaaaaatat	tatggaccac	acaaaatga			1179

<210> 189
 <211> 666
 <212> DNA
 <213> E. Coli

<400> 189

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atataa						666

<210> 190
 <211> 705
 <212> DNA
 <213> E. Coli

<400> 190

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ggtattatct	ttgctttgac	agttaagccc	agaactgaaa	gtcaagtcgg	aaaaatcccg	660
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<210> 191
 <211> 285
 <212> DNA
 <213> E. Coli

<400> 191

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<210> 192
 <211> 1977
 <212> DNA
 <213> E. Coli

[illegible][illegible][illegible]

Figure 1

Figure 1

Figure 1

Figure 1

Figure 1

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<210> 194

<211> 1572

<212> DNA

<213> E. Coli

<400> 194

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<210> 195
 <211> 1140
 <212> DNA
 <213> E. Coli

<400> 195

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<210> 196
 <211> 1371
 <212> DNA
 <213> E. Coli

<400> 196

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<210> 197

<211> 186

<212> DNA

<213> E. Coli

<400> 197

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tactaa						186

<210> 198

<211> 93

<212> DNA

<213> E. Coli

<400> 198

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gcatccgggg	ttcgaatccc	cgcctcaccg	cca			93

<210> 199

<211> 603

<212> DNA

<213> E. Coli

<400> 199

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atccaggatt	atcttgggca	tcgcaatatt	cgtcatactg	tctggtatac	cgccagcaat	540
gcagggcgtt	tttacggcat	ctgggataga	gccagaggac	gacagcgta	cgctgtttta	600
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<210> 200

<211> 597

<212> DNA

<213> E. Coli

<400> 200

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<210> 201
 <211> 549
 <212> DNA
 <213> E. Coli

<400> 201						
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<210> 202
 <211> 648
 <212> DNA
 <213> E. Coli

<400> 202						
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tcaggctcta	cttcgctaca	tttcacgccc	aaatatcgtg	ctaccggggc	tcgggttact	600
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<210> 203
 <211> 726
 <212> DNA
 <213> E. Coli

<400> 203						
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gaataa

726

<210> 204
<211> 2637
<212> DNA
<213> E. Coli

<400> 204

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<210> 205
<211> 531
<212> DNA
<213> E. Coli

<400> 205
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ccgggtaaac caatacgtc gaatttttac gcccggttaa tggcgacaca ggtgcctgtc 480
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<210> 206

<211> 504

<212> DNA

<213> E. Coli

<400> 206
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<210> 207

<211> 903

<212> DNA

<213> E. Coli

<400> 207
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<210> 208

<211> 1631

<212> DNA

<213> E. Coli

<400> 208

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<210> 209

<211> 534

<212> DNA

<213> E. Coli

<400> 209

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tcgacgtttt	ataagcggct	gaatgctggg	gatcgtaaag	gtgcatgcga	agcgattcgc	420
tgggtgatta	aggatggcgg	acgcgattgc	cgcatctcgt	caaataactg	ttacggctcag	480
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<210> 210

<211> 312

<212> DNA

<213> E. Coli

<400> 210

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<210> 211
 <211> 291
 <212> DNA
 <213> E. Coli

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 tcggcggggta atgctgggtt ctgggcattg cagttactcg ataaagtaac tccgtcacag 180
 tgggctgcaa tcgggtgtgct gggtagcctg gtttttgcc tgctgacgta tctgacaaat 240
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<210> 212
 <211> 216
 <212> DNA
 <213> E. Coli

<400> 212
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 aattatcgaa ccttatttga aggtcaaaag gttaccttct ctatagagag tgggtgctaaa 180
 ggtcctgcag cagcaaatgt catcattact gattaa 216

<210> 213
 <211> 1017
 <212> DNA
 <213> E. Coli

<400> 213
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<210> 214
 <211> 474
 <212> DNA
 <213> E. Coli

<400> 214
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ggctttggtc	ataataataa	tattgcggtg	gcgtatgtaa	aggaaaaata	tagaccgcga	240
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gatgaagcga	aatctttaca	tgattattcc	gtaagaaaat	ttcctgtgct	ttctgatttt	420
attgtgtcat	ttatgttagg	gattaaggaa	ggtgcgaaca	agtcctgat	atga	474

<210> 215
 <211> 1119
 <212> DNA
 <213> E. Coli

<400> 215

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gtccattctg	ctaaagagtt	aaaagaaaag	tatccatggg	ttaaattcat	tgagtttcct	180
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cgtgaaattc	ttatggagcc	tagctttttc	ttatttaaaa	tgctatacgg	gctgatata	420
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<210> 216
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 <212> DNA
 <213> E. Coli

<400> 216

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aaaatcataa	agaaatacaa	tcatgagacc	aaattatggg	aaaaagcata	g	591

<210> 217
 <211> 993
 <212> DNA
 <213> E. Coli

<400> 217

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ggtggagtag	tccagagaat	tattagttct	gttaagctta	gtacatttct	ctgcggtctt	180
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gagaatacaa	aaattatttc	tcagaaaatt	cgaacaggaa	gttacttcag	ggatgttctt	960
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<210> 218

<211> 1167

<212> DNA

<213> E. Coli

<400> 218

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<210> 219

<211> 1104

<212> DNA

<213> E. Coli

<400> 219

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<210> 220

<211> 1116

<212> DNA

<213> E. Coli

<400> 220

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<210> 221

<211> 1404

<212> DNA

<213> E. Coli

<400> 221

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gacaacggca	ccatcaacta	tgatcaggat	gttaacggca	tcatggtcgg	tggtgatacc	720
aaaattgacg	gtaacaacgc	taagtggatc	gtcgggtcgg	ctgcaggctt	cgctaaaggt	780

gacatgaatg	accgtttctgg	tcaggtggat	caagacagcc	agactgccta	catctactct	840
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gcctataccg	atgctaacta	cctcgggtgg	ggtgacgtag	atcaagactg	gtccgcgaac	1380
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<210> 222

<211> 669

<212> DNA

<213> E. Coli

<400> 222

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aaacctcttc	aggaatttgg	taagctcgat	aaatgtttgt	ccagatacgg	tacgcgcttc	120
gagtttaata	atgaaaagca	agttatat	tccagtgatg	tcaataacga	agatactttc	180
gttatttttag	aggagattat	ctctctgcgt	agagaagaaa	acgtacttat	cgggtattacc	240
caggctcctt	atattatggg	gctggctgat	ggtttaatga	aaaacgatat	accatacaaa	300
ttaatatcag	aaggaaattg	tacgggatat	catctaccag	ccaaacaaac	cattacgctt	360
attgaacaaa	atcaactctg	gcgagacgct	ttttactggg	tagcctggca	aaatagaatt	420
ctggaattac	gcgacgtgca	gctcattggg	cataattcct	acgaacaaat	ccgcgcaaca	480
ttattatcaa	tgattgactg	gaatgaagaa	ttgcgatcac	gtattgggtg	gatgaattat	540
atccatcaac	gtacacgcat	atcgcgcttc	gtcgtcgcag	aagttctcgc	tgctttgcgt	600
aaaggcggct	atatcgaaat	gaataaaggc	aaactggtcg	ctatcaaccg	tttgccttca	660
gagtattaa						669

<210> 223

<211> 255

<212> DNA

<213> E. Coli

<400> 223

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attgttggtg	ctatcgaaacg	ttttgtgaaa	cacccgatct	acggtaaatt	catcaagcgt	120
acgaccaaac	tgacagtaca	tgacgagaac	aacgaatgcg	gtatcgggtga	cgtgggttgaa	180
atccgcgaat	gccgtccgct	gtccaagact	aaatcctgga	cgctgggttcg	cgttgtagag	240
aaagcgggttc	tgtaa					255

<210> 224

<211> 192

<212> DNA

<213> E. Coli

<400> 224

atgaaagcaa	aagagctgcg	tgagaagagc	gttgaagagc	tgaacaccga	gctgctgaac	60
ctgctgctg	agcagttcaa	cctgcgtatg	caggctgcaa	gtggccagct	gcaacagtct	120
cacctgttga	agcaagtgcg	tcgcgatgtc	gcacgcgtta	agactttact	gaacgagaag	180
gcgggtgcgt	aa					192

<210> 225

<211> 411

<212> DNA

<213> E. Coli

<400> 225

atgtttacaac	caaagcgtac	aaaattccgt	aaaatgcaca	aaggccgtaa	ccgcgggtctg	60
gcgcagggta	cggatgttag	cttcggcagc	ttcgggtctga	aagctgttgg	ccgtgggtcgt	120
ctgactgccc	gtcagatcga	agcagcacgt	cgtgctatga	cccgtgcagt	taagcgtcaa	180
ggtaagatct	ggatccgtgt	gttcccggac	aaaccgatca	ctgaaaagcc	gctggcagtg	240
cgtatgggta	aaggtaaagg	taacgtggag	tattgggttg	ccttgattca	gccgggtaaa	300
gtcctgtatg	aaatggacgg	tgttccggaa	gagctggccc	gtgaagcatt	caagctggca	360
gcagcgaaac	tgccgattaa	aaccaccttt	gtaactaaga	cggatgatga	a	411

<210> 226

<211> 702

<212> DNA

<213> E. Coli

<400> 226

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acctggtttg	cgaacaccaa	agaattcgct	gacaacctgg	acagcgattt	taaagtacgt	120
cagtacctga	ctaaggaact	ggctaaagcg	tccgtatctc	gtatcgttat	cgagcgtccg	180
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ggatgaagac	tagaaaaact	gcgtaaggtc	gtagcggaca	tcgctggcgt	tcctgcacag	300
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gcaatgcgtc	tgggcgctaa	aggtattaaa	gttgaagtta	gcggccgtct	gggcggcgcg	480
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tggatcttca	aaggcgagat	cctgggtggg	atggctgctg	ttgaacaacc	ggaaaaaccg	660
gctgctcagc	ctaaaaagca	gcagcgtaaa	ggccgtaaat	aa		702

<210> 227

<211> 333

<212> DNA

<213> E. Coli

<400> 227

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aagaaagcgg	ctgtactggt	caagaaagtt	ctggaatctg	ccattgctaa	cgctgaacac	180
aacgatggcg	ctgacattga	cgatctgaaa	gttacgaaaa	ttttcgtaga	cgaaggccc	240
agcatgaagc	gcattatgcc	gcgtgcaaaa	ggctcgtcag	atcgcatcct	gaagcgcacc	300
agccacatca	ctgtggttgt	gtccgatcgc	tga			333

<210> 228

<211> 279

<212> DNA

<213> E. Coli

<400> 228

atgccacgtt	ctctcaagaa	aggtcctttt	attgacctgc	acttgctgaa	gaaggtagag	60
aaagcgggtg	aaagcggaga	caagaagccc	ctgcgcactt	ggccccgtcg	ttcaacgatc	120
tttcctaaca	tgatcggttt	gaccatcgct	gtccataatg	gtcgtcagca	cgttccggta	180
tttgtaaccg	acgaaatggt	tggtcacaaa	ctgggtgaat	tcgcaccgac	tcgtacttat	240
cgcggccacg	ctgctgataa	aaaagcgaag	aagaaataa			279

<210> 229

<211> 822

<212> DNA

<213> E. Coli

<400> 229

atggcagttg	ttaaagttaa	accgacatct	ccgggtcgtc	gccacgtagt	taaagtgggt	60
aaccctgagc	tgcacaaggg	caaacctttt	gctccgttgc	tggaaaaaaa	cagcaaatcc	120
ggtggtcgta	acaacaatgg	ccgtatcacc	actcgtcata	tcggtgggtg	ccacaagcag	180
gcttaccgta	ttgttgactt	caaacgcaac	aaagacggta	tcccggcagt	tgttgaacgt	240
cttgagtacg	atccgaaccg	ttccgcgaac	atcgcgctgg	ttctgtacaa	agacggtgaa	300
cgccgttaca	tcctggcccc	taaaggcctg	aaagctggcg	accagattca	gtctggcgtt	360
gatgctgcaa	tcaaaccagg	taacacctg	ccgatgcgca	acatcccggg	tggttctact	420
gttcataacg	tagaaatgaa	accaggtaaa	ggcggtcagc	tggcacgttc	cgctgggtact	480
tacgttcaga	tcgttgctcg	tgatggtgct	tatgtcacc	tgcgtctgcg	ttctggtgaa	540
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cgcggtaccg	cgatgaaccc	ggtagaccac	ccacatgggtg	gtggtgaagg	tcgtaacttt	720
ggtaagcacc	cggttaactcc	gtggggcggt	cagaccaaag	gtaagaagac	ccgcagcaac	780
aagcgtactg	ataaattcat	cgtacgtcgc	cgtagcaaat	aa		822

<210> 230

<211> 303

<212> DNA

<213> E. Coli

<400> 230

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gcagaaatca	aagctgctgt	gcagaaactg	tttgaagtgc	aagtcgaagt	cgtaaacacc	180
ctggtagtta	aagggaaagt	taaacgtcac	ggacagcgta	tcggtcgtcg	tagcgactgg	240
aaaaaagctt	acgtcaccct	gaaagaaggc	cagaatctgg	acttcgttgg	cggcgtgag	300
taa						303

<210> 231

<211> 630

<212> DNA

<213> E. Coli

<400> 231

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tctatcccag	taaccgtaat	cgaagttgaa	gcaaaccgcg	ttactcaggt	taaagacctg	120
gctaaccgatg	gctaccgtgc	tattcagggtg	accaccgggtg	ctaaaaaagc	taaccgtgtg	180
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cgcgttccgg	gttctatcgg	tcagaaccag	actccgggca	aagtgttcaa	aggcaagaaa	480
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gacgctgagc	gcaacctgct	gctggttaaa	ggtgctgtcc	cgggtgcaac	cggtagcgac	600
ctgatcggtta	aaccagctgt	gaaggcgtaa				630

<210> 232

<211> 606

<212> DNA

<213> E. Coli

<400> 232

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gagccgcccgg	tttgtcgtat	aatggattac	ggcaaattcc	tctatgaaaa	gagcaagtct	240
tctaaggaac	agaagaaaaa	gcaaaaagtt	atccagggtta	aggaaattaa	attccgtcct	300
ggtacagatg	aaggcgacta	tcaggtaaaaa	ctccgcagcc	tgattcgctt	tctcgaagag	360
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taa						543

<210> 237
 <211> 1929
 <212> DNA
 <213> E. Coli

<400> 237

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atggatgttg	cgctggacat	tggtccaggt	ctggcgaaaag	cctgtatcgc	agggcgcggtt	120
aatggcgaaac	tggttgatgc	ttgcgatctg	attgaaaacg	acgcacaact	gtcgaatcatt	180
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gggtttttatt	acgacgttga	tcttgaccgc	acgttaaccc	aggaagatgt	cgaagcactc	360
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gaggaataa						1929

<210> 238
 <211> 1353
 <212> DNA
 <213> E. Coli

<400> 238

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acctgcgtaa	atgttggtg	tgtgccgaaa	aaagtgatgt	ggcacgcggc	gcaaactcgt	180

gaagcgatcc	atatgtacgg	cccgattat	ggttttgata	ccactatcaa	taaattcaac	240
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aagattgtcg	gtattcacgg	cattggcttt	ggtatggacg	aaatgttgca	gggcttcgcg	1260
gtggcgctga	agatgggggc	aacccaaaaa	gacttcgaca	ataccgtcgc	cattcaccca	1320
acggcggcag	aagagtctgt	gacaatgcgt	taa			1353

<210> 239

<211> 2904

<212> DNA

<213> E. Coli

<400> 239

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cccggcctat	caacgtcgtc	gtcttcaacg	ttccttcagg	acccttaaag	ggtcagggag	120
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ttgtttccct	cttcacgacg	gacgttagca	cccgccgtgt	gtctcccgtg	ataacattct	1980
ccggtattcg	cagtttgcag	cgggttggtg	agtcgggatg	acccccttgc	cgaaacagtg	2040
ctctaccccc	ggagatgaat	tcacgaggcg	ctacctaaat	agctttcggg	gagaaccagc	2100
tatctcccgg	tttgattggc	ctttcacccc	cagccacaag	tcatccgcta	atttttcaac	2160
attagtcggg	tcggtcctcc	agttagtgtt	acccaacctt	caacctgccc	atggctagat	2220
caccgggttt	cgggtctata	ccctgcaact	taacgccag	ttaagactcg	gtttcccttc	2280
ggctccccta	ttcgggttaac	cttgctacag	aataaagtc	gctgacccat	tatacaaaag	2340
gtacgcagtc	acacgcctaa	gcgtgctccc	actgcttgta	cgtacacggg	ttcaggttct	2400
ttttcactcc	cctcgccggg	gttcttttcg	cctttccctc	acggtactgg	ttcactatcg	2460
gtcagtcagg	agtatttagc	cttgaggatg	ggcccccca	tattcagaca	ggataccacg	2520
tgtcccgcgc	tactcatcga	gctcacagca	tgtgcatttt	tgtgtacggg	gctgtcacc	2580
tgtatcgcg	gcctttccag	acgcttccac	taacacacac	actgattcag	gctctgggct	2640
gctccccgtt	cgctcgccgc	tactggggga	atctcggttg	atttcttttc	ctcgggggtac	2700
ttagatgttt	cagttccccc	ggttcgccct	attaacctat	ggattcagtt	aatgatagt	2760
tgtcgaaaca	cactgggttt	ccccattcgg	aaatcgccgg	ttataacggg	tcatatcacc	2820
ttaccgacgc	ttatcgacga	ttagcacgtc	cttcacgcgc	tctgactgcc	agggcatcca	2880
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<210> 240
 <211> 120
 <212> DNA
 <213> E. Coli

<400> 240						
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gtttcacttc	tgagttcggc	atggggtcag	gtgggaccac	cgcgctacgg	ccgccaggca	120

<210> 241
 <211> 76
 <212> DNA
 <213> E. Coli

<400> 241						
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cccctagggg	acgcca					76

<210> 242
 <211> 1549
 <212> DNA
 <213> E. Coli

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gtcgaacggg	aacaggaagc	agcttgctgc	ttcgctgacg	agtggcggac	gggtgagtaa	120
tgtctgggaa	gctgcctgat	ggagggggat	aactactgga	aacggtagct	aataccgcag	180
aatgtcgcaa	gaccaaagag	ggggaccttc	gggcctcttg	ccatcgcatg	tgcccagatg	240
ggattagctt	gttgggtggg	taacggctca	ccaaggcgac	gatccctagc	tggtctgaga	300
ggatgaccag	ccacactgga	actgagacac	ggtccagact	cctacgggag	gcagcagtg	360
ggaatattgc	acaatgggag	caagcctgat	gcagccatgc	cgcgtgtatg	aagaaggcct	420
tcggttggtg	aagtactttc	agcgggggag	aagggaagta	agttaatacc	tttgctcatt	480
gacgttaccc	gcagaagaag	caccggctaa	ctccgtgcc	gcagccgcgg	taatacggag	540
gggtgcaagc	ttaatcggaa	ttactgggag	taaagcgac	gcaggcgggt	tggttaagtc	600
agatgtgaaa	tccccgggct	caacctggga	actgcatctg	atactggcaa	gcttgagtct	660
cgtagagggg	ggtagaattc	caggtgtagc	ggtgaaatgc	gtagagatct	ggaggaatac	720
cgggtggcgaa	ggcgcccccc	tggacgaaga	ctgacgctca	ggtgcgaaag	cgtggggagc	780

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aaacaggatt agataccctg gtagtccacg ccgtaaacga tgtcgacttg gaggttgtgc      840
ccttgaggcg tggcttccgg agctaacgcg ttaagtcgac cgcctgggga gtacggccgc      900
aagggttaaaa ctcaaataaa ttgacggggg cccgcacaag cggtgaggca tgtggtttaa      960
ttcgatgcaa cgcgaagaac cttacctggg cttgacatcc acggaagttt tcagagatga     1020
gaatgtgcct tcgggaaccg tgagacaggt gctgcatggc tgtcgtcagc tcgtgttgtg     1080
aaatgttggg ttaagtcccg caacgagcgc aacccttatc ctttgttgcc agcgggccgg     1140
ccgggaactc aaaggagact gccagtata aactggagga aggtggggat gacgtcaagt     1200
catcatggcc cttacgacca gggctacaca cgtgctacaa tggcgcatac aaagagaagc     1260
gacctcgcgga gagcaagcgg acctcataaa gtgctgctga gtccggattg gagtctgcaa     1320
ctcgactcca tgaagtcgga atcgctagta atcggtggatc agaatgccac ggtgaatacg     1380
ttcccgggcc ttgtacacac cgcccgtcac accatgggag tgggttgcaa aagaagtagg     1440
tagcttaacc ttcggggagg cgcttaccac tttgtgattc atgactgggg tgaagtcgta     1500
acaaggtaac cgtaggggaa cctgcggttg gatcacctcc ttaccttaa     1549

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<210> 243

<211> 221

<212> PRT

<213> E. Coli

<400> 243

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Met Asn Val Phe Ser Gln Thr Gln Arg Tyr Lys Ala Leu Phe Trp Leu
 1          5          10          15
Ser Leu Phe His Leu Leu Val Ile Thr Ser Ser Asn Tyr Leu Val Gln
 20          25          30
Leu Pro Val Ser Ile Leu Gly Phe His Thr Thr Trp Gly Ala Phe Ser
 35          40          45
Phe Pro Phe Ile Phe Leu Ala Thr Asp Leu Thr Val Arg Ile Phe Gly
 50          55          60
Ala Pro Leu Ala Arg Arg Ile Ile Phe Ala Val Met Ile Pro Ala Leu
 65          70          75          80
Leu Ile Ser Tyr Val Ile Ser Ser Leu Phe Tyr Met Gly Ser Trp Gln
 85          90          95
Gly Phe Gly Ala Leu Ala His Phe Asn Leu Phe Val Ala Arg Ile Ala
 100          105          110
Thr Ala Ser Phe Met Ala Tyr Ala Leu Gly Gln Ile Leu Asp Val His
 115          120          125
Val Phe Asn Arg Leu Arg Gln Ser Arg Arg Trp Trp Leu Ala Pro Thr
 130          135          140
Ala Ser Thr Leu Phe Gly Asn Val Ser Asp Thr Leu Ala Phe Phe Phe
 145          150          155          160
Ile Ala Phe Trp Arg Ser Pro Asp Ala Phe Met Ala Glu His Trp Met
 165          170          175
Glu Ile Ala Leu Val Asp Tyr Cys Phe Lys Val Leu Ile Ser Ile Val
 180          185          190
Phe Phe Leu Pro Met Tyr Gly Val Leu Leu Asn Met Leu Leu Lys Arg
 195          200          205
Leu Ala Asp Lys Ser Glu Ile Asn Ala Leu Gln Ala Ser
 210          215          220

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<210> 244

<211> 203

<212> PRT

<213> E. Coli

<400> 244

Met	Ile	Arg	Trp	Met	Asn	Glu	Pro	Leu	Trp	Pro	Phe	Ile	Glu	Arg	Lys
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Lys	Ser	Met	Arg	Asn	Leu	Val	Lys	Tyr	Val	Gly	Ile	Gly	Leu	Leu	Val
			20					25					30		
Met	Gly	Leu	Ala	Ala	Cys	Asp	Asp	Lys	Asp	Thr	Asn	Ala	Thr	Ala	Gln
		35					40					45			
Gly	Ser	Val	Ala	Glu	Ser	Asn	Ala	Thr	Gly	Asn	Pro	Val	Asn	Leu	Leu
	50					55					60				
Asp	Gly	Lys	Leu	Ser	Phe	Ser	Leu	Pro	Ala	Asp	Met	Thr	Asp	Gln	Ser
65					70					75				80	
Gly	Lys	Leu	Gly	Thr	Gln	Ala	Asn	Asn	Met	His	Val	Trp	Ser	Asp	Ala
				85					90					95	
Thr	Gly	Gln	Lys	Ala	Val	Ile	Val	Ile	Met	Gly	Asp	Asp	Pro	Lys	Glu
			100					105					110		
Asp	Leu	Ala	Val	Leu	Ala	Lys	Arg	Leu	Glu	Asp	Gln	Gln	Arg	Ser	Arg
		115					120					125			
Asp	Pro	Gln	Leu	Gln	Val	Val	Thr	Asn	Lys	Ala	Ile	Glu	Leu	Lys	Gly
	130					135					140				
His	Lys	Met	Gln	Gln	Leu	Asp	Ser	Ile	Ile	Ser	Ala	Lys	Gly	Gln	Thr
145					150					155				160	
Ala	Tyr	Ser	Ser	Val	Ile	Leu	Gly	Asn	Val	Gly	Asn	Gln	Leu	Leu	Thr
				165				170						175	
Met	Gln	Ile	Thr	Leu	Pro	Ala	Asp	Asp	Gln	Gln	Lys	Ala	Gln	Thr	Thr
			180					185					190		
Ala	Glu	Asn	Ile	Ile	Asn	Thr	Leu	Val	Ile	Gln					
		195					200								

<210> 245

<211> 324

<212> PRT

<213> E. Coli

<400> 245

Met	Ala	Asn	Met	Phe	Ala	Leu	Ile	Leu	Val	Ile	Ala	Thr	Leu	Val	Thr
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Gly	Ile	Leu	Trp	Cys	Val	Asp	Lys	Phe	Phe	Phe	Ala	Pro	Lys	Arg	Arg
			20					25					30		
Glu	Arg	Gln	Ala	Ala	Ala	Gln	Ala	Ala	Ala	Gly	Asp	Ser	Leu	Asp	Lys
		35					40					45			
Ala	Thr	Leu	Lys	Lys	Val	Ala	Pro	Lys	Pro	Gly	Trp	Leu	Glu	Thr	Gly
	50					55					60				
Ala	Ser	Val	Phe	Pro	Val	Leu	Ala	Ile	Val	Leu	Ile	Val	Arg	Ser	Phe
65					70					75				80	
Ile	Tyr	Glu	Pro	Phe	Gln	Ile	Pro	Ser	Gly	Ser	Met	Met	Pro	Thr	Leu
				85					90					95	
Leu	Ile	Gly	Asp	Phe	Ile	Leu	Val	Glu	Lys	Phe	Ala	Tyr	Gly	Ile	Lys
			100					105					110		
Asp	Pro	Ile	Tyr	Gln	Lys	Thr	Leu	Ile	Glu	Thr	Gly	His	Pro	Lys	Arg
		115					120					125			
Gly	Asp	Ile	Val	Val	Phe	Lys	Tyr	Pro	Glu	Asp	Pro	Lys	Leu	Asp	Tyr
	130					135					140				
Ile	Lys	Arg	Ala	Val	Gly	Leu	Pro	Gly	Asp	Lys	Val	Thr	Tyr	Asp	Pro
145					150					155				160	
Val	Ser	Lys	Glu	Leu	Thr	Ile	Gln	Pro	Gly	Cys	Ser	Ser	Gly	Gln	Ala
				165					170					175	
Cys	Glu	Asn	Ala	Leu	Pro	Val	Thr	Tyr	Ser	Asn	Val	Glu	Pro	Ser	Asp

225					230					235					240
Ala	Glu	Ser	Val	Thr	Gln	Trp	Cys	Arg	Trp	Val	Thr	Phe	Thr	Ala	Arg
				245					250					255	
His	Asn	His	Leu	Pro	Ala	Pro	Gly	Ala	Asp	Ala	Trp	Pro	Ile	Leu	Ile
			260					265					270		
Arg	Glu	Ala	Ala	Arg	Tyr	Thr	Gly	Glu	Gln	Glu	Thr	Leu	Pro	Leu	Ser
		275					280					285			
Pro	Gln	Trp	Ile	Leu	Arg	Gln	Cys	Lys	Glu	Val	Ala	Ser	Leu	Cys	Asp
	290					295				300					
Gly	Asp	Thr	Phe	Ser	Gly	Glu	Gln	Leu	Asn	Leu	Met	Leu	Gln	Gln	Arg
305					310					315					320
Glu	Trp	Arg	Glu	Gly	Phe	Leu	Ala	Glu	Arg	Met	Gln	Asp	Glu	Ile	Leu
				325					330					335	
Gln	Glu	Gln	Ile	Leu	Ile	Glu	Thr	Glu	Gly	Glu	Arg	Ile	Gly	Gln	Ile
			340					345					350		
Asn	Ala	Leu	Ser	Val	Ile	Glu	Phe	Pro	Gly	His	Pro	Arg	Ala	Phe	Gly
		355					360					365			
Glu	Pro	Ser	Arg	Ile	Ser	Cys	Val	Val	His	Ile	Gly	Asp	Gly	Glu	Phe
	370					375					380				
Thr	Asp	Ile	Glu	Arg	Lys	Ala	Glu	Leu	Gly	Gly	Asn	Ile	His	Ala	Lys
385					390					395					400
Gly	Met	Met	Ile	Met	Gln	Ala	Phe	Leu	Met	Ser	Glu	Leu	Gln	Leu	Glu
				405					410					415	
Gln	Gln	Ile	Pro	Phe	Ser	Ala	Ser	Leu	Thr	Phe	Glu	Gln	Ser	Tyr	Ser
			420					425					430		
Glu	Val	Asp	Gly	Asp	Ser	Ala	Ser	Met	Ala	Glu	Leu	Cys	Ala	Leu	Ile
		435					440					445			
Ser	Ala	Leu	Ala	Asp	Val	Pro	Val	Asn	Gln	Ser	Ile	Ala	Ile	Thr	Gly
	450					455					460				
Ser	Val	Asp	Gln	Phe	Gly	Arg	Ala	Gln	Pro	Val	Gly	Gly	Leu	Asn	Glu
465					470					475					480
Lys	Ile	Glu	Gly	Phe	Phe	Ala	Ile	Cys	Gln	Gln	Arg	Glu	Leu	Thr	Gly
				485					490					495	
Lys	Gln	Gly	Val	Ile	Ile	Pro	Thr	Ala	Asn	Val	Arg	His	Leu	Ser	Leu
			500					505					510		
His	Ser	Glu	Leu	Val	Lys	Ala	Val	Glu	Glu	Gly	Lys	Phe	Thr	Ile	Trp
		515					520					525			
Ala	Val	Asp	Asp	Val	Thr	Asp	Ala	Leu	Pro	Leu	Leu	Leu	Asn	Leu	Val
	530					535					540				
Trp	Asp	Gly	Glu	Gly	Gln	Thr	Thr	Leu	Met	Gln	Thr	Ile	Gln	Glu	Arg
545					550					555					560
Ile	Ala	Gln	Ala	Ser	Gln	Gln	Glu	Gly	Arg	His	Arg	Phe	Pro	Trp	Pro
				565					570					575	
Leu	Arg	Trp	Leu	Asn	Trp	Phe	Ile	Pro	Asn						
			580					585							

<210> 247
 <211> 394
 <212> PRT
 <213> E. Coli

<400> 247															
Met	Ser	Lys	Glu	Lys	Phe	Glu	Arg	Thr	Lys	Pro	His	Val	Asn	Val	Gly
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Thr	Ile	Gly	His	Val	Asp	His	Gly	Lys	Thr	Thr	Leu	Thr	Ala	Ala	Ile
			20					25					30		

Thr	Thr	Val	Leu	Ala	Lys	Thr	Tyr	Gly	Gly	Ala	Ala	Arg	Ala	Phe	Asp
	35						40					45			
Gln	Ile	Asp	Asn	Ala	Pro	Glu	Glu	Lys	Ala	Arg	Gly	Ile	Thr	Ile	Asn
	50					55					60				
Thr	Ser	His	Val	Glu	Tyr	Asp	Thr	Pro	Thr	Arg	His	Tyr	Ala	His	Val
65					70					75				80	
Asp	Cys	Pro	Gly	His	Ala	Asp	Tyr	Val	Lys	Asn	Met	Ile	Thr	Gly	Ala
				85					90					95	
Ala	Gln	Met	Asp	Gly	Ala	Ile	Leu	Val	Val	Ala	Ala	Thr	Asp	Gly	Pro
			100					105					110		
Met	Pro	Gln	Thr	Arg	Glu	His	Ile	Leu	Leu	Gly	Arg	Gln	Val	Gly	Val
		115					120					125			
Pro	Tyr	Ile	Ile	Val	Phe	Leu	Asn	Lys	Cys	Asp	Met	Val	Asp	Asp	Glu
	130					135					140				
Glu	Leu	Leu	Glu	Leu	Val	Glu	Met	Glu	Val	Arg	Glu	Leu	Leu	Ser	Gln
145					150					155					160
Tyr	Asp	Phe	Pro	Gly	Asp	Asp	Thr	Pro	Ile	Val	Arg	Gly	Ser	Ala	Leu
				165					170					175	
Lys	Ala	Leu	Glu	Gly	Asp	Ala	Glu	Trp	Glu	Ala	Lys	Ile	Leu	Glu	Leu
			180					185					190		
Ala	Gly	Phe	Leu	Asp	Ser	Tyr	Ile	Pro	Glu	Pro	Glu	Arg	Ala	Ile	Asp
		195					200					205			
Lys	Pro	Phe	Leu	Leu	Pro	Ile	Glu	Asp	Val	Phe	Ser	Ile	Ser	Gly	Arg
	210					215					220				
Gly	Thr	Val	Val	Thr	Gly	Arg	Val	Glu	Arg	Gly	Ile	Ile	Lys	Val	Gly
225					230					235					240
Glu	Glu	Val	Glu	Ile	Val	Gly	Ile	Lys	Glu	Thr	Gln	Lys	Ser	Thr	Cys
				245					250					255	
Thr	Gly	Val	Glu	Met	Phe	Arg	Lys	Leu	Leu	Asp	Glu	Gly	Arg	Ala	Gly
			260					265					270		
Glu	Asn	Val	Gly	Val	Leu	Leu	Arg	Gly	Ile	Lys	Arg	Glu	Glu	Ile	Glu
		275					280					285			
Arg	Gly	Gln	Val	Leu	Ala	Lys	Pro	Gly	Thr	Ile	Lys	Pro	His	Thr	Lys
	290					295					300				
Phe	Glu	Ser	Glu	Val	Tyr	Ile	Leu	Ser	Lys	Asp	Glu	Gly	Gly	Arg	His
305					310					315					320
Thr	Pro	Phe	Phe	Lys	Gly	Tyr	Arg	Pro	Gln	Phe	Tyr	Phe	Arg	Thr	Thr
				325					330					335	
Asp	Val	Thr	Gly	Thr	Ile	Glu	Leu	Pro	Glu	Gly	Val	Glu	Met	Val	Met
			340					345					350		
Pro	Gly	Asp	Asn	Ile	Lys	Met	Val	Val	Thr	Leu	Ile	His	Pro	Ile	Ala
		355					360					365			
Met	Asp	Asp	Gly	Leu	Arg	Phe	Ala	Ile	Arg	Glu	Gly	Gly	Arg	Thr	Val
	370					375					380				
Gly	Ala	Gly	Val	Val	Ala	Lys	Val	Leu	Gly						
385					390										

<210> 248

<211> 704

<212> PRT

<213> E. Coli

<400> 248

Met	Ala	Arg	Thr	Thr	Pro	Ile	Ala	Arg	Tyr	Arg	Asn	Ile	Gly	Ile	Ser
1				5					10					15	

Ala	His	Ile	Asp	Ala	Gly	Lys	Thr	Thr	Thr	Thr	Glu	Arg	Ile	Leu	Phe
			20					25					30		
Tyr	Thr	Gly	Val	Asn	His	Lys	Ile	Gly	Glu	Val	His	Asp	Gly	Ala	Ala
		35					40					45			
Thr	Met	Asp	Trp	Met	Glu	Gln	Glu	Gln	Glu	Arg	Gly	Ile	Thr	Ile	Thr
		50				55					60				
Ser	Ala	Ala	Thr	Thr	Ala	Phe	Trp	Ser	Gly	Met	Ala	Lys	Gln	Tyr	Glu
65					70				75						80
Pro	His	Arg	Ile	Asn	Ile	Ile	Asp	Thr	Pro	Gly	His	Val	Asp	Phe	Thr
				85					90					95	
Ile	Glu	Val	Glu	Arg	Ser	Met	Arg	Val	Leu	Asp	Gly	Ala	Val	Met	Val
			100					105					110		
Tyr	Cys	Ala	Val	Gly	Gly	Val	Gln	Pro	Gln	Ser	Glu	Thr	Val	Trp	Arg
		115					120					125			
Gln	Ala	Asn	Lys	Tyr	Lys	Val	Pro	Arg	Ile	Ala	Phe	Val	Asn	Lys	Met
		130				135					140				
Asp	Arg	Met	Gly	Ala	Asn	Phe	Leu	Lys	Val	Val	Asn	Gln	Ile	Lys	Thr
145					150					155					160
Arg	Leu	Gly	Ala	Asn	Pro	Val	Pro	Leu	Gln	Leu	Ala	Ile	Gly	Ala	Glu
				165					170					175	
Glu	His	Phe	Thr	Gly	Val	Val	Asp	Leu	Val	Lys	Met	Lys	Ala	Ile	Asn
			180					185					190		
Trp	Asn	Asp	Ala	Asp	Gln	Gly	Val	Thr	Phe	Glu	Tyr	Glu	Asp	Ile	Pro
		195					200					205			
Ala	Asp	Met	Val	Glu	Leu	Ala	Asn	Glu	Trp	His	Gln	Asn	Leu	Ile	Glu
		210				215					220				
Ser	Ala	Ala	Glu	Ala	Ser	Glu	Glu	Leu	Met	Glu	Lys	Tyr	Leu	Gly	Gly
225					230					235					240
Glu	Glu	Leu	Thr	Glu	Ala	Glu	Ile	Lys	Gly	Ala	Leu	Arg	Gln	Arg	Val
				245					250					255	
Leu	Asn	Asn	Glu	Ile	Ile	Leu	Val	Thr	Cys	Gly	Ser	Ala	Phe	Lys	Asn
			260					265					270		
Lys	Gly	Val	Gln	Ala	Met	Leu	Asp	Ala	Val	Ile	Asp	Tyr	Leu	Pro	Ser
		275					280					285			
Pro	Val	Asp	Val	Pro	Ala	Ile	Asn	Gly	Ile	Leu	Asp	Asp	Gly	Lys	Asp
		290				295					300				
Thr	Pro	Ala	Glu	Arg	His	Ala	Ser	Asp	Asp	Glu	Pro	Phe	Ser	Ala	Leu
305					310					315					320
Ala	Phe	Lys	Ile	Ala	Thr	Asp	Pro	Phe	Val	Gly	Asn	Leu	Thr	Phe	Phe
				325					330					335	
Arg	Val	Tyr	Ser	Gly	Val	Val	Asn	Ser	Gly	Asp	Thr	Val	Leu	Asn	Ser
			340					345					350		
Val	Lys	Ala	Ala	Arg	Glu	Arg	Phe	Gly	Arg	Ile	Val	Gln	Met	His	Ala
			355				360					365			
Asn	Lys	Arg	Glu	Glu	Ile	Lys	Glu	Val	Arg	Ala	Gly	Asp	Ile	Ala	Ala
			370			375					380				
Ala	Ile	Gly	Leu	Lys	Asp	Val	Thr	Thr	Gly	Asp	Thr	Leu	Cys	Asp	Pro
385					390					395					400
Asp	Ala	Pro	Ile	Ile	Leu	Glu	Arg	Met	Glu	Phe	Pro	Glu	Pro	Val	Ile
				405					410					415	
Ser	Ile	Ala	Val	Glu	Pro	Lys	Thr	Lys	Ala	Asp	Gln	Glu	Lys	Met	Gly
			420					425					430		
Leu	Ala	Leu	Gly	Arg	Leu	Ala	Lys	Glu	Asp	Pro	Ser	Phe	Arg	Val	Trp
			435				440					445			
Thr	Asp	Glu	Glu	Ser	Asn	Gln	Thr	Ile	Ile	Ala	Gly	Met	Gly	Glu	Leu
	450					455					460				
His	Leu	Asp	Ile	Ile	Val	Asp	Arg	Met	Lys	Arg	Glu	Phe	Asn	Val	Glu

465		470		475		480
Ala Asn Val Gly Lys Pro Gln Val Ala Tyr Arg Glu Thr Ile Arg Gln						
	485		490		495	
Lys Val Thr Asp Val Glu Gly Lys His Ala Lys Gln Ser Gly Gly Arg						
	500		505		510	
Gly Gln Tyr Gly His Val Val Ile Asp Met Tyr Pro Leu Glu Pro Gly						
	515		520		525	
Ser Asn Pro Lys Gly Tyr Glu Phe Ile Asn Asp Ile Lys Gly Gly Val						
	530		535		540	
Ile Pro Gly Glu Tyr Ile Pro Ala Val Asp Lys Gly Ile Gln Glu Gln						
	545		550		555	
Leu Lys Ala Gly Pro Leu Ala Gly Tyr Pro Val Val Asp Met Gly Ile						
	565		570		575	
Arg Leu His Phe Gly Ser Tyr His Asp Val Asp Ser Ser Glu Leu Ala						
	580		585		590	
Phe Lys Leu Ala Ala Ser Ile Ala Phe Lys Glu Gly Phe Lys Lys Ala						
	595		600		605	
Lys Pro Val Leu Leu Glu Pro Ile Met Lys Val Glu Val Glu Thr Pro						
	610		615		620	
Glu Glu Asn Thr Gly Asp Val Ile Gly Asp Leu Ser Arg Arg Arg Gly						
	625		630		635	
Met Leu Lys Gly Gln Glu Ser Glu Val Thr Gly Val Lys Ile His Ala						
	645		650		655	
Glu Val Pro Leu Ser Glu Met Phe Gly Tyr Ala Thr Gln Leu Arg Ser						
	660		665		670	
Leu Thr Lys Gly Arg Ala Ser Tyr Thr Met Glu Phe Leu Lys Tyr Asp						
	675		680		685	
Glu Ala Pro Ser Asn Val Ala Gln Ala Val Ile Glu Ala Arg Gly Lys						
	690		695		700	

<210> 249

<211> 179

<212> PRT

<213> E. Coli

<400> 249

Met Pro Arg Arg Arg Val Ile Gly Gln Arg Lys Ile Leu Pro Asp Pro						
1	5	10	15			
Lys Phe Gly Ser Glu Leu Leu Ala Lys Phe Val Asn Ile Leu Met Val						
	20	25	30			
Asp Gly Lys Lys Ser Thr Ala Glu Ser Ile Val Tyr Ser Ala Leu Glu						
	35	40	45			
Thr Leu Ala Gln Arg Ser Gly Lys Ser Glu Leu Glu Ala Phe Glu Val						
	50	55	60			
Ala Leu Glu Asn Val Arg Pro Thr Val Glu Val Lys Ser Arg Arg Val						
	65	70	75		80	
Gly Gly Ser Thr Tyr Gln Val Pro Val Glu Val Arg Pro Val Arg Arg						
	85	90	95			
Asn Ala Leu Ala Met Arg Trp Ile Val Glu Ala Ala Arg Lys Arg Gly						
	100	105	110			
Asp Lys Ser Met Ala Leu Arg Leu Ala Asn Glu Leu Ser Asp Ala Ala						
	115	120	125			
Glu Asn Lys Gly Thr Ala Val Lys Lys Arg Glu Asp Val His Arg Met						
	130	135	140			
Ala Glu Ala Asn Lys Ala Phe Ala His Tyr Arg Trp Leu Ser Leu Arg						
	145	150	155		160	

Ser Phe Ser His Gln Ala Gly Ala Ser Ser Lys Gln Pro Ala Leu Gly
 165 170 175
 Tyr Leu Asn

<210> 250
 <211> 124
 <212> PRT
 <213> E. Coli

<400> 250

Met Ala Thr Val Asn Gln Leu Val Arg Lys Pro Arg Ala Arg Lys Val
 1 5 10 15
 Ala Lys Ser Asn Val Pro Ala Leu Glu Ala Cys Pro Gln Lys Arg Gly
 20 25 30
 Val Cys Thr Arg Val Tyr Thr Thr Thr Pro Lys Lys Pro Asn Ser Ala
 35 40 45
 Leu Arg Lys Val Cys Arg Val Arg Leu Thr Asn Gly Phe Glu Val Thr
 50 55 60
 Ser Tyr Ile Gly Gly Glu Gly His Asn Leu Gln Glu His Ser Val Ile
 65 70 75 80
 Leu Ile Arg Gly Gly Arg Val Lys Asp Leu Pro Gly Val Arg Tyr His
 85 90 95
 Thr Val Arg Gly Ala Leu Asp Cys Ser Gly Val Lys Asp Arg Lys Gln
 100 105 110
 Ala Arg Ser Lys Tyr Gly Val Lys Arg Pro Lys Ala
 115 120

<210> 251
 <211> 165
 <212> PRT
 <213> E. Coli

<400> 251

Met Ala Leu Asn Leu Gln Asp Lys Gln Ala Ile Val Ala Glu Val Ser
 1 5 10 15
 Glu Val Ala Lys Gly Ala Leu Ser Ala Val Val Ala Asp Ser Arg Gly
 20 25 30
 Val Thr Val Asp Lys Met Thr Glu Leu Arg Lys Ala Gly Arg Glu Ala
 35 40 45
 Gly Val Tyr Met Arg Val Val Arg Asn Thr Leu Leu Arg Arg Ala Val
 50 55 60
 Glu Gly Thr Pro Phe Glu Cys Leu Lys Asp Ala Phe Val Gly Pro Thr
 65 70 75 80
 Leu Ile Ala Tyr Ser Met Glu His Pro Gly Ala Ala Ala Arg Leu Phe
 85 90 95
 Lys Glu Phe Ala Lys Ala Asn Ala Lys Phe Glu Val Lys Ala Ala Ala
 100 105 110
 Phe Glu Gly Glu Leu Ile Pro Ala Ser Gln Ile Asp Arg Leu Ala Thr
 115 120 125
 Leu Pro Thr Tyr Glu Glu Ala Ile Ala Arg Leu Met Ala Thr Met Lys
 130 135 140
 Glu Ala Ser Ala Gly Lys Leu Val Arg Thr Leu Ala Ala Val Arg Asp
 145 150 155 160
 Ala Lys Glu Ala Ala

<210> 252
 <211> 121
 <212> PRT
 <213> E. Coli

<400> 252

Met	Ser	Ile	Thr	Lys	Asp	Gln	Ile	Ile	Glu	Ala	Val	Ala	Ala	Met	Ser
1				5					10					15	
Val	Met	Asp	Val	Val	Glu	Leu	Ile	Ser	Ala	Met	Glu	Glu	Lys	Phe	Gly
			20					25					30		
Val	Ser	Ala	Ala	Ala	Ala	Val	Ala	Val	Ala	Ala	Gly	Pro	Val	Glu	Ala
		35				40					45				
Ala	Glu	Glu	Lys	Thr	Glu	Phe	Asp	Val	Ile	Leu	Lys	Ala	Ala	Gly	Ala
	50					55					60				
Asn	Lys	Val	Ala	Val	Ile	Lys	Ala	Val	Arg	Gly	Ala	Thr	Gly	Leu	Gly
65					70				75					80	
Leu	Lys	Glu	Ala	Lys	Asp	Leu	Val	Glu	Ser	Ala	Pro	Ala	Ala	Leu	Lys
				85				90						95	
Glu	Gly	Val	Ser	Lys	Asp	Asp	Ala	Glu	Ala	Leu	Lys	Lys	Ala	Leu	Glu
			100					105					110		
Glu	Ala	Gly	Ala	Glu	Val	Glu	Val	Lys							
		115						120							

<210> 253
 <211> 714
 <212> PRT
 <213> E. Coli

<400> 253

Met	Ser	Arg	Ile	Ile	Met	Leu	Ile	Pro	Thr	Gly	Thr	Ser	Val	Gly	Leu
1				5					10					15	
Thr	Ser	Val	Ser	Leu	Gly	Val	Ile	Arg	Ala	Met	Glu	Arg	Lys	Gly	Val
			20					25					30		
Arg	Leu	Ser	Val	Phe	Lys	Pro	Ile	Ala	Gln	Pro	Arg	Thr	Gly	Gly	Asp
		35				40						45			
Ala	Pro	Asp	Gln	Thr	Thr	Thr	Ile	Val	Arg	Ala	Asn	Ser	Ser	Thr	Thr
	50					55					60				
Thr	Ala	Ala	Glu	Pro	Leu	Lys	Met	Ser	Tyr	Val	Glu	Gly	Leu	Leu	Ser
65					70				75					80	
Ser	Asn	Gln	Lys	Asp	Val	Leu	Met	Glu	Glu	Ile	Val	Ala	Asn	Tyr	His
			85					90					95		
Ala	Asn	Thr	Lys	Asp	Ala	Glu	Val	Val	Leu	Val	Glu	Gly	Leu	Val	Pro
		100						105					110		
Thr	Arg	Lys	His	Gln	Phe	Ala	Gln	Ser	Leu	Asn	Tyr	Glu	Ile	Ala	Lys
		115					120					125			
Thr	Leu	Asn	Ala	Glu	Ile	Val	Phe	Val	Met	Ser	Gln	Gly	Thr	Asp	Thr
	130					135					140				
Pro	Glu	Gln	Leu	Lys	Glu	Arg	Ile	Glu	Leu	Thr	Arg	Asn	Ser	Phe	Gly
145					150					155					160
Gly	Ala	Lys	Asn	Thr	Asn	Ile	Thr	Gly	Val	Ile	Val	Asn	Lys	Leu	Asn
			165					170						175	
Ala	Pro	Val	Asp	Glu	Gln	Gly	Arg	Thr	Arg	Pro	Asp	Leu	Ser	Glu	Ile
			180					185					190		

Phe	Asp	Asp	Ser	Ser	Lys	Ala	Lys	Val	Asn	Asn	Val	Asp	Pro	Ala	Lys
	195						200					205			
Leu	Gln	Glu	Ser	Ser	Pro	Leu	Pro	Val	Leu	Gly	Ala	Val	Pro	Trp	Ser
	210					215					220				
Phe	Asp	Leu	Ile	Ala	Thr	Arg	Ala	Ile	Asp	Met	Ala	Arg	His	Leu	Asn
225					230				235						240
Ala	Thr	Ile	Ile	Asn	Glu	Gly	Asp	Ile	Asn	Thr	Arg	Arg	Val	Lys	Ser
				245					250					255	
Val	Thr	Phe	Cys	Ala	Arg	Ser	Ile	Pro	His	Met	Leu	Glu	His	Phe	Arg
			260					265					270		
Ala	Gly	Ser	Leu	Leu	Val	Thr	Ser	Ala	Asp	Arg	Pro	Asp	Val	Leu	Val
		275					280					285			
Ala	Ala	Cys	Leu	Ala	Ala	Met	Asn	Gly	Val	Glu	Ile	Gly	Ala	Leu	Leu
	290					295					300				
Leu	Thr	Gly	Gly	Tyr	Glu	Met	Asp	Ala	Arg	Ile	Ser	Lys	Leu	Cys	Glu
305					310					315					320
Arg	Ala	Phe	Ala	Thr	Gly	Leu	Pro	Val	Phe	Met	Val	Asn	Thr	Asn	Thr
				325					330					335	
Trp	Gln	Thr	Ser	Leu	Ser	Leu	Gln	Ser	Phe	Asn	Leu	Glu	Val	Pro	Val
			340					345					350		
Asp	Asp	His	Glu	Arg	Ile	Glu	Lys	Val	Gln	Glu	Tyr	Val	Ala	Asn	Tyr
		355					360					365			
Ile	Asn	Ala	Asp	Trp	Ile	Glu	Ser	Leu	Thr	Ala	Thr	Ser	Glu	Arg	Ser
	370					375					380				
Arg	Arg	Leu	Ser	Pro	Pro	Ala	Phe	Arg	Tyr	Gln	Leu	Thr	Glu	Leu	Ala
385					390					395					400
Arg	Lys	Ala	Gly	Lys	Arg	Ile	Val	Leu	Pro	Glu	Gly	Asp	Glu	Pro	Arg
				405					410					415	
Thr	Val	Lys	Ala	Ala	Ala	Ile	Cys	Ala	Glu	Arg	Gly	Ile	Ala	Thr	Cys
			420					425					430		
Val	Leu	Leu	Gly	Asn	Pro	Ala	Glu	Ile	Asn	Arg	Val	Ala	Ala	Ser	Gln
		435					440					445			
Gly	Val	Glu	Leu	Gly	Ala	Gly	Ile	Glu	Ile	Val	Asp	Pro	Glu	Val	Val
	450					455					460				
Arg	Glu	Ser	Tyr	Val	Gly	Arg	Leu	Val	Glu	Leu	Arg	Lys	Asn	Lys	Gly
465					470					475					480
Met	Thr	Glu	Thr	Val	Ala	Arg	Glu	Gln	Leu	Glu	Asp	Asn	Val	Val	Leu
				485					490					495	
Gly	Thr	Leu	Met	Leu	Glu	Gln	Asp	Glu	Val	Asp	Gly	Leu	Val	Ser	Gly
			500					505					510		
Ala	Val	His	Thr	Thr	Ala	Asn	Thr	Ile	Arg	Pro	Pro	Leu	Gln	Leu	Ile
		515					520					525			
Lys	Thr	Ala	Pro	Gly	Ser	Ser	Leu	Val	Ser	Ser	Val	Phe	Phe	Met	Leu
	530					535					540				
Leu	Pro	Glu	Gln	Val	Tyr	Val	Tyr	Gly	Asp	Cys	Ala	Ile	Asn	Pro	Asp
545					550					555					560
Pro	Thr	Ala	Glu	Gln	Leu	Ala	Glu	Ile	Ala	Ile	Gln	Ser	Ala	Asp	Ser
				565					570					575	
Ala	Ala	Ala	Phe	Gly	Ile	Glu	Pro	Arg	Val	Ala	Met	Leu	Ser	Tyr	Ser
			580					585					590		
Thr	Gly	Thr	Ser	Gly	Ala	Gly	Ser	Asp	Val	Glu	Lys	Val	Arg	Glu	Ala
			595				600					605			
Thr	Arg	Leu	Ala	Gln	Glu	Lys	Arg	Pro	Asp	Leu	Met	Ile	Asp	Gly	Pro
	610					615					620				
Leu	Gln	Tyr	Asp	Ala	Ala	Val	Met	Ala	Asp	Val	Ala	Lys	Ser	Lys	Ala
625					630					635					640
Pro	Asn	Ser	Pro	Val	Ala	Gly	Arg	Ala	Thr	Val	Phe	Ile	Phe	Pro	Asp

				645					650				655			
Leu	Asn	Thr	Gly	Asn	Thr	Thr	Tyr	Lys	Ala	Val	Gln	Arg	Ser	Ala	Asp	
			660					665					670			
Leu	Ile	Ser	Ile	Gly	Pro	Met	Leu	Gln	Gly	Met	Arg	Lys	Pro	Val	Asn	
			675				680					685				
Asp	Leu	Ser	Arg	Gly	Ala	Leu	Val	Asp	Asp	Ile	Val	Tyr	Thr	Ile	Ala	
	690					695					700					
Leu	Thr	Ala	Ile	Gln	Ser	Ala	Gln	Gln	Gln							
705					710											

<210> 254

<211> 588

<212> PRT

<213> E. Coli

<400> 254

Met	Asn	Asn	Ser	Ile	Asn	His	Lys	Phe	His	His	Ile	Ser	Arg	Ala	Glu	
1				5				10						15		
Tyr	Gln	Glu	Leu	Leu	Ala	Val	Ser	Arg	Gly	Asp	Ala	Val	Ala	Asp	Tyr	
			20					25					30			
Ile	Ile	Asp	Asn	Val	Ser	Ile	Leu	Asp	Leu	Ile	Asn	Gly	Gly	Glu	Ile	
		35					40					45				
Ser	Gly	Pro	Ile	Val	Ile	Lys	Gly	Arg	Tyr	Ile	Ala	Gly	Val	Gly	Ala	
	50					55					60					
Glu	Tyr	Thr	Asp	Ala	Pro	Ala	Leu	Gln	Arg	Ile	Asp	Ala	Arg	Gly	Ala	
65				70					75						80	
Thr	Ala	Val	Pro	Gly	Phe	Ile	Asp	Ala	His	Leu	His	Ile	Glu	Ser	Ser	
			85					90						95		
Met	Met	Thr	Pro	Val	Thr	Phe	Glu	Thr	Ala	Thr	Leu	Pro	Arg	Gly	Leu	
			100					105					110			
Thr	Thr	Val	Ile	Cys	Asp	Pro	His	Glu	Ile	Val	Asn	Val	Met	Gly	Glu	
		115					120					125				
Ala	Gly	Phe	Ala	Trp	Phe	Ala	Arg	Cys	Ala	Glu	Gln	Ala	Arg	Gln	Asn	
	130					135					140					
Gln	Tyr	Leu	Gln	Val	Ser	Ser	Cys	Val	Pro	Ala	Leu	Glu	Gly	Cys	Asp	
145				150					155					160		
Val	Asn	Gly	Ala	Ser	Phe	Thr	Leu	Glu	Gln	Met	Leu	Ala	Trp	Arg	Asp	
			165					170						175		
His	Pro	Gln	Val	Thr	Gly	Leu	Ala	Glu	Met	Met	Asp	Tyr	Pro	Gly	Val	
		180						185					190			
Ile	Ser	Gly	Gln	Asn	Ala	Leu	Leu	Asp	Lys	Leu	Asp	Ala	Phe	Arg	His	
		195				200						205				
Leu	Thr	Leu	Asp	Gly	His	Cys	Pro	Gly	Leu	Gly	Gly	Lys	Glu	Leu	Asn	
	210				215						220					
Ala	Tyr	Ile	Thr	Ala	Gly	Ile	Glu	Asn	Cys	His	Glu	Ser	Tyr	Gln	Leu	
225				230					235						240	
Glu	Glu	Gly	Arg	Arg	Lys	Leu	Gln	Leu	Gly	Met	Ser	Leu	Met	Ile	Arg	
			245					250						255		
Glu	Gly	Ser	Ala	Ala	Arg	Asn	Leu	Asn	Ala	Leu	Ala	Pro	Leu	Ile	Asn	
			260				265						270			
Glu	Phe	Asn	Ser	Pro	Gln	Cys	Met	Leu	Cys	Thr	Asp	Asp	Arg	Asn	Pro	
	275					280						285				
Trp	Glu	Ile	Ala	His	Glu	Gly	His	Ile	Asp	Ala	Leu	Ile	Arg	Arg	Leu	
	290				295						300					
Ile	Glu	Gln	His	Asn	Val	Pro	Leu	His	Val	Ala	Tyr	Arg	Val	Ala	Ser	
305					310					315					320	

Trp	Ser	Thr	Ala	Arg	His	Phe	Gly	Leu	Asn	His	Leu	Gly	Leu	Leu	Ala
				325					330					335	
Pro	Gly	Lys	Gln	Ala	Asp	Ile	Val	Leu	Leu	Ser	Asp	Ala	Arg	Lys	Val
			340					345					350		
Thr	Val	Gln	Gln	Val	Leu	Val	Lys	Gly	Glu	Pro	Ile	Asp	Ala	Gln	Thr
		355					360					365			
Leu	Gln	Ala	Glu	Glu	Ser	Ala	Arg	Leu	Ala	Gln	Ser	Ala	Pro	Pro	Tyr
	370					375					380				
Gly	Asn	Thr	Ile	Ala	Arg	Gln	Pro	Val	Ser	Ala	Ser	Asp	Phe	Ala	Leu
385					390					395					400
Gln	Phe	Thr	Pro	Gly	Lys	Arg	Tyr	Arg	Val	Ile	Asp	Val	Ile	His	Asn
			405						410					415	
Glu	Leu	Ile	Thr	His	Ser	His	Ser	Ser	Val	Tyr	Ser	Glu	Asn	Gly	Phe
		420						425					430		
Asp	Arg	Asp	Asp	Val	Ser	Phe	Ile	Ala	Val	Leu	Glu	Arg	Tyr	Gly	Gln
		435					440					445			
Arg	Leu	Ala	Pro	Ala	Cys	Gly	Leu	Leu	Gly	Gly	Phe	Gly	Leu	Asn	Glu
	450					455					460				
Gly	Ala	Leu	Ala	Ala	Thr	Val	Ser	His	Asp	Ser	His	Asn	Ile	Val	Val
465					470				475						480
Ile	Gly	Arg	Ser	Ala	Glu	Glu	Met	Ala	Leu	Ala	Val	Asn	Gln	Val	Ile
				485					490					495	
Gln	Asp	Gly	Gly	Gly	Leu	Cys	Val	Val	Arg	Asn	Gly	Gln	Val	Gln	Ser
			500					505					510		
His	Leu	Pro	Leu	Pro	Ile	Ala	Gly	Leu	Met	Ser	Thr	Asp	Thr	Ala	Gln
		515					520					525			
Ser	Leu	Ala	Glu	Gln	Ile	Asp	Ala	Leu	Lys	Ala	Ala	Ala	Arg	Glu	Cys
	530					535					540				
Gly	Pro	Leu	Pro	Asp	Glu	Pro	Phe	Ile	Gln	Met	Ala	Phe	Leu	Ser	Leu
545					550					555					560
Pro	Val	Ile	Pro	Ala	Leu	Lys	Leu	Thr	Ser	Gln	Gly	Leu	Phe	Asp	Gly
				565					570					575	
Glu	Lys	Phe	Ala	Phe	Thr	Thr	Leu	Glu	Val	Thr	Glu				
			580					585							

<210> 255

<211> 408

<212> PRT

<213> E. Coli

<400> 255

Met	Ala	Tyr	Cys	Asn	Pro	Gly	Leu	Glu	Ser	Arg	Pro	Asn	Lys	Arg	Asn
1				5					10					15	
Ala	Leu	Arg	Arg	His	Val	Val	Thr	Gly	Ile	Gly	Met	Lys	Ile	Val	Ile
		20						25					30		
Ala	Pro	Asp	Ser	Tyr	Lys	Glu	Ser	Leu	Ser	Ala	Ser	Glu	Val	Ala	Gln
		35					40					45			
Ala	Ile	Glu	Lys	Gly	Phe	Arg	Glu	Ile	Phe	Pro	Asp	Ala	Gln	Tyr	Val
	50					55					60				
Ser	Val	Pro	Val	Ala	Asp	Gly	Gly	Glu	Gly	Thr	Val	Glu	Ala	Met	Ile
65					70					75					80
Ala	Ala	Thr	Gln	Gly	Ala	Glu	Arg	His	Ala	Trp	Val	Thr	Gly	Pro	Leu
			85						90					95	
Gly	Glu	Lys	Val	Asn	Ala	Ser	Trp	Gly	Ile	Ser	Gly	Asp	Gly	Lys	Thr
			100					105					110		
Ala	Phe	Ile	Glu	Met	Ala	Ala	Ala	Ser	Gly	Leu	Glu	Leu	Val	Pro	Ala

Asp	Met	Ser	Ser	Ile	Ala	Pro	Leu	Ala	Ser	Arg	Glu	Ile	Ser	Glu	Ala	
			100					105					110			
Leu	Lys	Ala	Lys	Gly	Ile	Asp	Met	Leu	Asp	Ala	Pro	Val	Ser	Gly	Gly	
		115					120					125				
Glu	Pro	Lys	Ala	Ile	Asp	Gly	Thr	Leu	Ser	Val	Met	Val	Gly	Gly	Asp	
		130				135					140					
Lys	Ala	Ile	Phe	Asp	Lys	Tyr	Tyr	Asp	Leu	Met	Lys	Ala	Met	Ala	Gly	
145					150				155						160	
Ser	Val	Val	His	Thr	Gly	Glu	Ile	Gly	Ala	Gly	Asn	Val	Thr	Lys	Leu	
				165					170					175		
Ala	Asn	Gln	Val	Ile	Val	Ala	Leu	Asn	Ile	Ala	Ala	Met	Ser	Glu	Ala	
			180					185					190			
Leu	Thr	Leu	Ala	Thr	Lys	Ala	Gly	Val	Asn	Pro	Asp	Leu	Val	Tyr	Gln	
		195					200					205				
Ala	Ile	Arg	Gly	Gly	Leu	Ala	Gly	Ser	Thr	Val	Leu	Asp	Ala	Lys	Ala	
		210				215					220					
Pro	Met	Val	Met	Asp	Arg	Asn	Phe	Lys	Pro	Gly	Phe	Arg	Ile	Asp	Leu	
225					230					235					240	
His	Ile	Lys	Asp	Leu	Ala	Asn	Ala	Leu	Asp	Thr	Ser	His	Gly	Val	Gly	
			245						250					255		
Ala	Gln	Leu	Pro	Leu	Thr	Ala	Ala	Val	Met	Glu	Met	Met	Gln	Ala	Leu	
			260					265					270			
Arg	Ala	Asp	Gly	Leu	Gly	Thr	Ala	Asp	His	Ser	Ala	Leu	Ala	Cys	Tyr	
		275					280					285				
Tyr	Glu	Lys	Leu	Ala	Lys	Val	Glu	Val	Thr	Arg						
	290					295										

<210> 257

<211> 256

<212> PRT

<213> E. Coli

<400> 257

Met	Asn	Asn	Asp	Val	Phe	Pro	Asn	Lys	Phe	Lys	Ala	Ala	Leu	Ala	Ala	
1				5				10					15			
Lys	Gln	Val	Gln	Ile	Gly	Cys	Trp	Ser	Ala	Leu	Ser	Asn	Pro	Ile	Ser	
			20					25					30			
Thr	Glu	Val	Leu	Gly	Leu	Ala	Gly	Phe	Asp	Trp	Leu	Val	Leu	Asp	Gly	
		35					40					45				
Glu	His	Ala	Pro	Asn	Asp	Ile	Ser	Thr	Phe	Ile	Pro	Gln	Leu	Met	Ala	
	50				55						60					
Leu	Lys	Gly	Ser	Ala	Ser	Ala	Pro	Val	Val	Arg	Val	Pro	Thr	Asn	Glu	
65					70					75					80	
Pro	Val	Ile	Ile	Lys	Arg	Leu	Leu	Asp	Ile	Gly	Phe	Tyr	Asn	Phe	Leu	
				85				90						95		
Ile	Pro	Phe	Val	Glu	Thr	Lys	Glu	Glu	Ala	Glu	Leu	Ala	Val	Ala	Ser	
			100					105					110			
Thr	Arg	Tyr	Pro	Pro	Glu	Gly	Ile	Arg	Gly	Val	Ser	Val	Ser	His	Arg	
		115					120					125				
Ala	Asn	Met	Phe	Gly	Thr	Val	Ala	Asp	Tyr	Phe	Ala	Gln	Ser	Asn	Lys	
		130				135					140					
Asn	Ile	Thr	Ile	Leu	Val	Gln	Ile	Glu	Ser	Gln	Gln	Gly	Val	Asp	Asn	
145					150					155					160	
Val	Asp	Ala	Ile	Ala	Ala	Thr	Glu	Gly	Val	Asp	Gly	Ile	Phe	Val	Gly	
				165					170					175		

Pro	Ser	Asp	Leu	Ala	Ala	Ala	Leu	Gly	His	Leu	Gly	Asn	Ala	Ser	His
			180					185				190			
Pro	Asp	Val	Gln	Lys	Ala	Ile	Gln	His	Ile	Phe	Asn	Arg	Ala	Ser	Ala
			195				200					205			
His	Gly	Lys	Pro	Ser	Gly	Ile	Leu	Ala	Pro	Val	Glu	Ala	Asp	Ala	Arg
			210			215					220				
Arg	Tyr	Leu	Glu	Trp	Gly	Ala	Thr	Phe	Val	Ala	Val	Gly	Ser	Asp	Leu
225					230					235					240
Gly	Val	Phe	Arg	Ser	Ala	Thr	Gln	Lys	Leu	Ala	Asp	Thr	Phe	Lys	Lys
				245					250					255	

<210> 258

<211> 444

<212> PRT

<213> E. Coli

<400> 258

Met	Ile	Leu	Asp	Thr	Val	Asp	Glu	Lys	Lys	Lys	Gly	Val	His	Thr	Arg
1				5				10						15	
Tyr	Leu	Ile	Leu	Leu	Ile	Ile	Phe	Ile	Val	Thr	Ala	Val	Asn	Tyr	Ala
			20					25					30		
Asp	Arg	Ala	Thr	Leu	Ser	Ile	Ala	Gly	Thr	Glu	Val	Ala	Lys	Glu	Leu
		35					40					45			
Gln	Leu	Ser	Ala	Val	Ser	Met	Gly	Tyr	Ile	Phe	Ser	Ala	Phe	Gly	Trp
	50					55					60				
Ala	Tyr	Leu	Leu	Met	Gln	Ile	Pro	Gly	Gly	Trp	Leu	Leu	Asp	Lys	Phe
65				70					75						80
Gly	Ser	Lys	Lys	Val	Tyr	Thr	Tyr	Ser	Leu	Phe	Phe	Trp	Ser	Leu	Phe
			85					90						95	
Thr	Phe	Leu	Gln	Gly	Phe	Val	Asp	Met	Phe	Pro	Leu	Ala	Trp	Ala	Gly
			100					105					110		
Ile	Ser	Met	Phe	Phe	Met	Arg	Phe	Met	Leu	Gly	Phe	Ser	Glu	Ala	Pro
		115					120					125			
Ser	Phe	Pro	Ala	Asn	Ala	Arg	Ile	Val	Ala	Ala	Trp	Phe	Pro	Thr	Lys
	130					135					140				
Glu	Arg	Gly	Thr	Ala	Ser	Ala	Ile	Phe	Asn	Ser	Ala	Gln	Tyr	Phe	Ser
145					150					155					160
Leu	Ala	Leu	Phe	Ser	Pro	Leu	Leu	Gly	Trp	Leu	Thr	Phe	Ala	Trp	Gly
				165					170					175	
Trp	Glu	His	Val	Phe	Thr	Val	Met	Gly	Val	Ile	Gly	Phe	Val	Leu	Thr
			180					185					190		
Ala	Leu	Trp	Ile	Lys	Leu	Ile	His	Asn	Pro	Thr	Asp	His	Pro	Arg	Met
		195					200					205			
Ser	Ala	Glu	Glu	Leu	Lys	Phe	Ile	Ser	Glu	Asn	Gly	Ala	Val	Val	Asp
	210					215					220				
Met	Asp	His	Lys	Lys	Pro	Gly	Ser	Ala	Ala	Ala	Ser	Gly	Pro	Lys	Leu
225					230					235					240
His	Tyr	Ile	Lys	Gln	Leu	Leu	Ser	Asn	Arg	Met	Met	Leu	Gly	Val	Phe
				245					250					255	
Phe	Gly	Gln	Tyr	Phe	Ile	Asn	Thr	Ile	Thr	Trp	Phe	Phe	Leu	Thr	Trp
			260					265					270		
Phe	Pro	Ile	Tyr	Leu	Val	Gln	Glu	Lys	Gly	Met	Ser	Ile	Leu	Lys	Val
		275					280					285			
Gly	Leu	Val	Ala	Ser	Ile	Pro	Ala	Leu	Cys	Gly	Phe	Ala	Gly	Gly	Val
	290					295					300				
Leu	Gly	Gly	Val	Phe	Ser	Asp	Tyr	Leu	Ile	Lys	Arg	Gly	Leu	Ser	Leu

305					310					315				320	
Thr	Leu	Ala	Arg	Lys	Leu	Pro	Ile	Val	Leu	Gly	Met	Leu	Leu	Ala	Ser
				325					330					335	
Thr	Ile	Ile	Leu	Cys	Asn	Tyr	Thr	Asn	Asn	Thr	Thr	Leu	Val	Val	Met
			340					345					350		
Leu	Met	Ala	Leu	Ala	Phe	Phe	Gly	Lys	Gly	Phe	Gly	Ala	Leu	Gly	Trp
		355					360					365			
Pro	Val	Ile	Ser	Asp	Thr	Ala	Pro	Lys	Glu	Ile	Val	Gly	Leu	Cys	Gly
	370					375					380				
Gly	Val	Phe	Asn	Val	Phe	Gly	Asn	Val	Ala	Ser	Ile	Val	Thr	Pro	Leu
	385				390					395					400
Val	Ile	Gly	Tyr	Leu	Val	Ser	Glu	Leu	His	Ser	Phe	Asn	Ala	Ala	Leu
				405					410					415	
Val	Phe	Val	Gly	Cys	Ser	Ala	Leu	Met	Ala	Met	Val	Cys	Tyr	Leu	Phe
			420					425					430		
Val	Val	Gly	Asp	Ile	Lys	Arg	Met	Glu	Leu	Gln	Lys				
		435					440								

<210> 259

<211> 511

<212> PRT

<213> E. Coli

<400> 259

Met	Gln	Thr	Ser	Asp	Thr	Arg	Ala	Leu	Pro	Leu	Leu	Cys	Ala	Arg	Ser
1				5					10					15	
Val	Tyr	Lys	Gln	Tyr	Ser	Gly	Val	Asn	Val	Leu	Lys	Gly	Ile	Asp	Phe
			20					25					30		
Thr	Leu	His	Gln	Gly	Glu	Val	His	Ala	Leu	Leu	Gly	Gly	Asn	Gly	Ala
		35					40					45			
Gly	Lys	Ser	Thr	Leu	Met	Lys	Ile	Ile	Ala	Gly	Ile	Thr	Pro	Ala	Asp
	50					55					60				
Ser	Gly	Thr	Leu	Glu	Ile	Glu	Gly	Asn	Asn	Tyr	Val	Arg	Leu	Thr	Pro
65				70						75					80
Val	His	Ala	His	Gln	Leu	Gly	Ile	Tyr	Leu	Val	Pro	Gln	Glu	Pro	Leu
				85					90					95	
Leu	Phe	Pro	Ser	Leu	Ser	Ile	Lys	Glu	Asn	Ile	Leu	Phe	Gly	Leu	Ala
			100					105					110		
Lys	Lys	Gln	Leu	Ser	Met	Gln	Lys	Met	Lys	Asn	Leu	Leu	Ala	Ala	Leu
		115					120					125			
Gly	Cys	Gln	Phe	Asp	Leu	His	Ser	Leu	Ala	Gly	Ser	Leu	Asp	Val	Ala
	130					135					140				
Asp	Arg	Gln	Met	Val	Glu	Ile	Leu	Arg	Gly	Leu	Met	Arg	Asp	Ser	Arg
145				150						155					160
Ile	Leu	Ile	Leu	Asp	Glu	Pro	Thr	Ala	Ser	Leu	Thr	Pro	Ala	Glu	Thr
				165					170					175	
Glu	Arg	Leu	Phe	Ser	Arg	Leu	Gln	Glu	Leu	Leu	Ala	Thr	Gly	Val	Gly
			180					185					190		
Ile	Val	Phe	Ile	Ser	His	Lys	Leu	Pro	Glu	Ile	Arg	Gln	Ile	Ala	Asp
		195					200					205			
Arg	Ile	Ser	Val	Met	Arg	Asp	Gly	Thr	Ile	Ala	Leu	Ser	Gly	Lys	Thr
	210					215					220				
Ser	Glu	Leu	Ser	Thr	Asp	Asp	Ile	Ile	Gln	Ala	Ile	Thr	Pro	Ala	Val
225				230						235					240
Arg	Glu	Lys	Ser	Leu	Ser	Ala	Ser	Gln	Lys	Leu	Trp	Leu	Glu	Leu	Pro
				245					250					255	

130	135	140
Pro Ala Glu Leu Lys Gln Leu Ser Ala Pro Leu Leu Leu Gly Val Ser		
145	150	155
Ala Ile Gly Trp Leu Thr Ile Ile Leu Val Ala Phe Met Ala Trp Leu		160
	165	170
Leu Ala Lys Thr Ala Phe Gly Arg Ser Phe Tyr Ala Thr Gly Asp Asn		175
	180	185
Leu Gln Gly Ala Arg Gln Leu Gly Val Arg Thr Glu Ala Ile Arg Ile		190
	195	200
Val Ala Phe Ser Leu Asn Gly Cys Met Ala Ala Leu Ala Gly Ile Val		205
	210	215
Phe Ala Ser Gln Ile Gly Phe Ile Pro Asn Gln Thr Gly Thr Gly Leu		220
225	230	235
Glu Met Lys Ala Ile Ala Ala Cys Val Leu Gly Gly Ile Ser Leu Leu		240
	245	250
Gly Gly Ser Gly Ala Ile Ile Gly Ala Val Leu Gly Ala Trp Phe Leu		255
	260	265
Thr Gln Ile Asp Ser Val Leu Val Leu Leu Arg Ile Pro Ala Trp Trp		270
	275	280
Asn Asp Phe Ile Ala Gly Leu Val Leu Leu Ala Val Leu Val Phe Asp		285
	290	295
Gly Arg Leu Arg Cys Ala Leu Glu Arg Asn Leu Arg Arg Gln Lys Tyr		300
305	310	315
Ala Arg Phe Met Thr Pro Pro Pro Ser Val Lys Pro Ala Ser Ser Gly		320
	325	330
Lys Lys Arg Glu Ala Ala		335
	340	

<210> 261
 <211> 330
 <212> PRT
 <213> E. Coli

<400> 261
Met Arg Ile Arg Tyr Gly Trp Glu Leu Ala Leu Ala Ala Leu Leu Val
1 5 10 15
Ile Glu Ile Val Ala Phe Gly Ala Ile Asn Pro Arg Met Leu Asp Leu
20 25 30
Asn Met Leu Leu Phe Ser Thr Ser Asp Phe Ile Cys Ile Gly Ile Val
35 40 45
Ala Leu Pro Leu Thr Met Val Ile Val Ser Gly Gly Ile Asp Ile Ser
50 55 60
Phe Gly Ser Thr Ile Gly Leu Cys Ala Ile Ala Leu Gly Val Leu Phe
65 70 75 80
Gln Ser Gly Val Pro Met Pro Leu Ala Ile Leu Leu Thr Leu Leu Leu
85 90 95
Gly Ala Leu Cys Gly Leu Ile Asn Ala Gly Leu Ile Ile Tyr Thr Lys
100 105 110
Val Asn Pro Leu Val Ile Thr Leu Gly Thr Leu Tyr Leu Phe Ala Gly
115 120 125
Ser Ala Leu Leu Leu Ser Gly Met Ala Gly Ala Thr Gly Tyr Glu Gly
130 135 140
Ile Gly Gly Phe Pro Met Ala Phe Thr Asp Phe Ala Asn Leu Asp Val
145 150 155 160
Leu Gly Leu Pro Val Pro Leu Ile Ile Phe Leu Ile Cys Leu Leu Val
165 170 175
Phe Trp Leu Trp Leu His Lys Thr His Ala Gly Arg Asn Val Phe Leu

				180					185				190				
Ile	Gly	Gln	Ser	Pro	Arg	Val	Ala	Leu	Tyr	Ser	Ala	Ile	Pro	Val	Asn		
		195					200					205					
Arg	Thr	Leu	Cys	Ala	Leu	Tyr	Ala	Met	Thr	Gly	Leu	Ala	Ser	Ala	Val		
	210					215					220						
Ala	Ala	Val	Leu	Leu	Val	Ser	Tyr	Phe	Gly	Ser	Ala	Arg	Ser	Asp	Leu		
225					230				235						240		
Gly	Ala	Ser	Phe	Leu	Met	Pro	Ala	Ile	Thr	Ala	Val	Val	Leu	Gly	Gly		
			245						250					255			
Ala	Asn	Ile	Tyr	Gly	Gly	Ser	Gly	Ser	Ile	Ile	Gly	Thr	Ala	Ile	Ala		
		260				265							270				
Val	Leu	Leu	Val	Gly	Tyr	Leu	Gln	Gly	Leu	Gln	Met	Ala	Gly	Val			
	275					280					285						
Pro	Asn	Gln	Val	Ser	Ser	Ala	Leu	Ser	Gly	Ala	Leu	Leu	Ile	Val	Val		
	290				295					300							
Val	Val	Gly	Arg	Ser	Val	Ser	Leu	His	Arg	Gln	Gln	Ile	Lys	Glu	Trp		
305				310					315						320		
Leu	Ala	Arg	Arg	Ala	Asn	Asn	Pro	Leu	Pro								
				325					330								

<210> 262
 <211> 340
 <212> PRT
 <213> E. Coli

Met	Thr	Leu	His	Arg	Phe	Lys	Lys	Ile	Ala	Leu	Leu	Ser	Ala	Leu	Gly		
1				5				10						15			
Ile	Ala	Ala	Ile	Ser	Met	Asn	Val	Gln	Ala	Ala	Glu	Arg	Ile	Ala	Phe		
		20						25					30				
Ile	Pro	Lys	Leu	Val	Gly	Val	Gly	Phe	Phe	Thr	Ser	Gly	Gly	Asn	Gly		
		35				40						45					
Ala	Gln	Gln	Ala	Gly	Lys	Glu	Leu	Gly	Val	Asp	Val	Thr	Tyr	Asp	Gly		
	50				55					60							
Pro	Thr	Glu	Pro	Ser	Val	Ser	Gly	Gln	Val	Gln	Leu	Ile	Asn	Asn	Phe		
65				70					75						80		
Val	Asn	Gln	Gly	Tyr	Asn	Ala	Ile	Ile	Val	Ser	Ala	Val	Ser	Pro	Asp		
			85					90						95			
Gly	Leu	Cys	Pro	Ala	Leu	Lys	Arg	Ala	Met	Gln	Arg	Gly	Val	Arg	Val		
		100					105						110				
Leu	Thr	Trp	Asp	Ser	Asp	Thr	Lys	Pro	Glu	Cys	Arg	Ser	Tyr	Tyr	Ile		
	115					120						125					
Asn	Gln	Gly	Thr	Pro	Ala	Gln	Leu	Gly	Gly	Met	Leu	Val	Asp	Met	Ala		
	130				135					140							
Ala	Arg	Gln	Val	Asn	Lys	Asp	Lys	Ala	Lys	Val	Ala	Phe	Phe	Tyr	Ser		
145				150					155						160		
Ser	Pro	Thr	Val	Thr	Asp	Gln	Asn	Gln	Trp	Val	Lys	Glu	Ala	Lys	Ala		
			165					170						175			
Lys	Ile	Ala	Lys	Glu	His	Pro	Gly	Trp	Glu	Ile	Val	Thr	Thr	Gln	Phe		
	180						185						190				
Gly	Tyr	Asn	Asp	Ala	Thr	Lys	Ser	Leu	Gln	Thr	Ala	Glu	Gly	Ile	Leu		
	195					200						205					
Lys	Ala	Tyr	Ser	Asp	Leu	Asp	Ala	Ile	Ile	Ala	Pro	Asp	Ala	Asn	Ala		
	210				215						220						

Leu	Pro	Ala	Ala	Ala	Gln	Ala	Ala	Glu	Asn	Leu	Lys	Asn	Asp	Lys	Val
225					230					235					240
Ala	Ile	Val	Gly	Phe	Ser	Thr	Pro	Asn	Val	Met	Arg	Pro	Tyr	Val	Glu
				245					250					255	
Arg	Gly	Thr	Val	Lys	Glu	Phe	Gly	Leu	Trp	Asp	Val	Val	Gln	Gln	Gly
			260					265					270		
Lys	Ile	Ser	Val	Tyr	Val	Ala	Asp	Ala	Leu	Leu	Lys	Lys	Gly	Ser	Met
	275						280					285			
Lys	Thr	Gly	Asp	Lys	Leu	Asp	Ile	Lys	Gly	Val	Gly	Gln	Val	Glu	Val
	290					295					300				
Ser	Pro	Asn	Ser	Val	Gln	Gly	Tyr	Asp	Tyr	Glu	Ala	Asp	Gly	Asn	Gly
305					310					315					320
Ile	Val	Leu	Leu	Pro	Glu	Arg	Val	Ile	Phe	Asn	Lys	Glu	Asn	Ile	Gly
				325					330					335	
Lys	Tyr	Asp	Phe												
			340												

<210> 263

<211> 291

<212> PRT

<213> E. Coli

<400> 263

Met	Ala	Asp	Leu	Asp	Asp	Ile	Lys	Asp	Gly	Lys	Asp	Phe	Arg	Thr	Asp
1				5					10					15	
Gln	Pro	Gln	Lys	Asn	Ile	Pro	Phe	Thr	Leu	Lys	Gly	Cys	Gly	Ala	Leu
			20					25					30		
Asp	Trp	Gly	Met	Gln	Ser	Arg	Leu	Ser	Arg	Ile	Phe	Asn	Pro	Lys	Thr
	35						40					45			
Gly	Lys	Thr	Val	Met	Leu	Ala	Phe	Asp	His	Gly	Tyr	Phe	Gln	Gly	Pro
	50					55					60				
Thr	Thr	Gly	Leu	Glu	Arg	Ile	Asp	Ile	Asn	Ile	Ala	Pro	Leu	Phe	Glu
65					70					75					80
His	Ala	Asp	Val	Leu	Met	Cys	Thr	Arg	Gly	Ile	Leu	Arg	Ser	Val	Val
				85					90					95	
Pro	Pro	Ala	Thr	Asn	Arg	Pro	Val	Val	Leu	Arg	Ala	Ser	Gly	Ala	Asn
			100					105					110		
Ser	Ile	Leu	Ala	Glu	Leu	Ser	Asn	Glu	Ala	Val	Ala	Leu	Ser	Met	Asp
	115						120					125			
Asp	Ala	Val	Arg	Leu	Asn	Ser	Cys	Ala	Val	Ala	Ala	Gln	Val	Tyr	Ile
	130					135					140				
Gly	Ser	Glu	Tyr	Glu	His	Gln	Ser	Ile	Lys	Asn	Ile	Ile	Gln	Leu	Val
145					150					155					160
Asp	Ala	Gly	Met	Lys	Val	Gly	Met	Pro	Thr	Met	Ala	Val	Thr	Gly	Val
			165						170					175	
Gly	Lys	Asp	Met	Val	Arg	Asp	Gln	Arg	Tyr	Phe	Ser	Leu	Ala	Thr	Arg
		180					185						190		
Ile	Ala	Ala	Glu	Met	Gly	Ala	Gln	Ile	Ile	Lys	Thr	Tyr	Tyr	Val	Glu
	195						200					205			
Lys	Gly	Phe	Glu	Arg	Ile	Val	Ala	Gly	Cys	Pro	Val	Pro	Ile	Val	Ile
	210					215					220				
Ala	Gly	Gly	Lys	Lys	Leu	Pro	Glu	Arg	Glu	Ala	Leu	Glu	Met	Cys	Trp
225					230					235					240
Gln	Ala	Ile	Asp	Gln	Gly	Ala	Ser	Gly	Val	Asp	Met	Gly	Arg	Asn	Ile
				245					250					255	
Phe	Gln	Ser	Asp	His	Pro	Val	Ala	Met	Met	Lys	Ala	Val	Gln	Ala	Val

260 265 270
 Val His His Asn Glu Thr Ala Asp Arg Ala Tyr Glu Leu Tyr Leu Ser
 275 280 285
 Glu Lys Gln
 290

<210> 264
 <211> 96
 <212> PRT
 <213> E. Coli

<400> 264
 Met His Val Thr Leu Val Glu Ile Asn Val His Glu Asp Lys Val Asp
 1 5 10 15
 Glu Phe Ile Glu Val Phe Arg Gln Asn His Leu Gly Ser Val Gln Glu
 20 25 30
 Glu Gly Asn Leu Arg Phe Asp Val Leu Gln Asp Pro Glu Val Asn Ser
 35 40 45
 Arg Phe Tyr Ile Tyr Glu Ala Tyr Lys Asp Glu Asp Ala Val Ala Phe
 50 55 60
 His Lys Thr Thr Pro His Tyr Lys Thr Cys Val Ala Lys Leu Glu Ser
 65 70 75 80
 Leu Met Thr Gly Pro Arg Lys Lys Arg Leu Phe Asn Gly Leu Met Pro
 85 90 95

<210> 265
 <211> 383
 <212> PRT
 <213> E. Coli

<400> 265
 Met Phe Glu Pro Met Glu Leu Thr Asn Asp Ala Val Ile Lys Val Ile
 1 5 10 15
 Gly Val Gly Gly Gly Gly Gly Asn Ala Val Glu His Met Val Arg Glu
 20 25 30
 Arg Ile Glu Gly Val Glu Phe Phe Ala Val Asn Thr Asp Ala Gln Ala
 35 40 45
 Leu Arg Lys Thr Ala Val Gly Gln Thr Ile Gln Ile Gly Ser Gly Ile
 50 55 60
 Thr Lys Gly Leu Gly Ala Gly Ala Asn Pro Glu Val Gly Arg Asn Ala
 65 70 75 80
 Ala Asp Glu Asp Arg Asp Ala Leu Arg Ala Ala Leu Glu Gly Ala Asp
 85 90 95
 Met Val Phe Ile Ala Ala Gly Met Gly Gly Gly Thr Gly Thr Gly Ala
 100 105 110
 Ala Pro Val Val Ala Glu Val Ala Lys Asp Leu Gly Ile Leu Thr Val
 115 120 125
 Ala Val Val Thr Lys Pro Phe Asn Phe Glu Gly Lys Lys Arg Met Ala
 130 135 140
 Phe Ala Glu Gln Gly Ile Thr Glu Leu Ser Lys His Val Asp Ser Leu
 145 150 155 160
 Ile Thr Ile Pro Asn Asp Lys Leu Leu Lys Val Leu Gly Arg Gly Ile
 165 170 175
 Ser Leu Leu Asp Ala Phe Gly Ala Ala Asn Asp Val Leu Lys Gly Ala
 180 185 190

Val	Gln	Gly	Ile	Ala	Glu	Leu	Ile	Thr	Arg	Pro	Gly	Leu	Met	Asn	Val
	195						200					205			
Asp	Phe	Ala	Asp	Val	Arg	Thr	Val	Met	Ser	Glu	Met	Gly	Tyr	Ala	Met
	210					215					220				
Met	Gly	Ser	Gly	Val	Ala	Ser	Gly	Glu	Asp	Arg	Ala	Glu	Glu	Ala	Ala
	225				230				235						240
Glu	Met	Ala	Ile	Ser	Ser	Pro	Leu	Leu	Glu	Asp	Ile	Asp	Leu	Ser	Gly
			245						250					255	
Ala	Arg	Gly	Val	Leu	Val	Asn	Ile	Thr	Ala	Gly	Phe	Asp	Leu	Arg	Leu
			260					265					270		
Asp	Glu	Phe	Glu	Thr	Val	Gly	Asn	Thr	Ile	Arg	Ala	Phe	Ala	Ser	Asp
	275					280						285			
Asn	Ala	Thr	Val	Val	Ile	Gly	Thr	Ser	Leu	Asp	Pro	Asp	Met	Asn	Asp
	290					295					300				
Glu	Leu	Arg	Val	Thr	Val	Ala	Thr	Gly	Ile	Gly	Met	Asp	Lys	Arg	
	305				310				315					320	
Pro	Glu	Ile	Thr	Leu	Val	Thr	Asn	Lys	Gln	Val	Gln	Gln	Pro	Val	Met
				325					330					335	
Asp	Arg	Tyr	Gln	Gln	His	Gly	Met	Ala	Pro	Leu	Thr	Gln	Glu	Gln	Lys
			340					345					350		
Pro	Val	Ala	Lys	Val	Val	Asn	Asp	Asn	Ala	Pro	Gln	Thr	Ala	Lys	Glu
		355					360					365			
Pro	Asp	Tyr	Leu	Asp	Ile	Pro	Ala	Phe	Leu	Arg	Lys	Gln	Ala	Asp	
	370					375					380				

<210> 266
 <211> 1014
 <212> PRT
 <213> E. Coli

<400> 266

Met	Asp	Val	Ser	Arg	Arg	Gln	Phe	Phe	Lys	Ile	Cys	Ala	Gly	Gly	Met
1			5					10					15		
Ala	Gly	Thr	Thr	Val	Ala	Ala	Leu	Gly	Phe	Ala	Pro	Lys	Gln	Ala	Leu
		20						25					30		
Ala	Gln	Ala	Arg	Asn	Tyr	Lys	Leu	Leu	Arg	Ala	Lys	Glu	Ile	Arg	Asn
		35					40					45			
Thr	Cys	Thr	Tyr	Cys	Ser	Val	Gly	Cys	Gly	Leu	Leu	Met	Tyr	Ser	Leu
	50				55					60					
Gly	Asp	Gly	Ala	Lys	Asn	Ala	Arg	Glu	Ala	Ile	Tyr	His	Ile	Glu	Gly
	65				70					75				80	
Asp	Pro	Asp	His	Pro	Val	Ser	Arg	Gly	Ala	Leu	Cys	Pro	Lys	Gly	Ala
			85					90					95		
Gly	Leu	Leu	Asp	Tyr	Val	Asn	Ser	Glu	Asn	Arg	Leu	Arg	Tyr	Pro	Glu
		100						105					110		
Tyr	Arg	Ala	Pro	Gly	Ser	Asp	Lys	Trp	Gln	Arg	Ile	Ser	Trp	Glu	Glu
		115					120					125			
Ala	Phe	Ser	Arg	Ile	Ala	Lys	Leu	Met	Lys	Ala	Asp	Arg	Asp	Ala	Asn
	130					135					140				
Phe	Ile	Glu	Lys	Asn	Glu	Gln	Gly	Val	Thr	Val	Asn	Arg	Trp	Leu	Ser
	145				150					155				160	
Thr	Gly	Met	Leu	Cys	Ala	Ser	Gly	Ala	Ser	Asn	Glu	Thr	Gly	Met	Leu
			165					170					175		
Thr	Gln	Lys	Phe	Ala	Arg	Ser	Leu	Gly	Met	Leu	Ala	Val	Asp	Asn	Gln
		180						185					190		
Ala	Arg	Val	His	Gly	Pro	Thr	Val	Ala	Ser	Leu	Ala	Pro	Thr	Phe	Gly

His	His	Leu	Arg	Glu	Leu	Tyr	Gln	Ser	Glu	Gly	Gly	Lys	Gly	Val	Glu		
			660					665					670				
Pro	Leu	Met	Lys	Met	Ser	Trp	Asn	Tyr	Lys	Gln	Pro	His	Glu	Pro	Gln		
		675					680					685					
Ser	Asp	Glu	Val	Ala	Lys	Glu	Asn	Asn	Gly	Tyr	Ala	Leu	Glu	Asp	Leu		
		690				695					700						
Tyr	Asp	Ala	Asn	Gly	Val	Leu	Ile	Ala	Lys	Lys	Gly	Gln	Leu	Leu	Ser		
705				710						715					720		
Ser	Phe	Ala	His	Leu	Arg	Asp	Asp	Gly	Thr	Thr	Ala	Ser	Ser	Cys	Trp		
			725					730						735			
Ile	Tyr	Thr	Gly	Ser	Trp	Thr	Glu	Gln	Gly	Asn	Gln	Met	Ala	Asn	Arg		
		740					745						750				
Asp	Asn	Ser	Asp	Pro	Ser	Gly	Leu	Gly	Asn	Thr	Leu	Gly	Trp	Ala	Trp		
		755				760					765						
Ala	Trp	Pro	Leu	Asn	Arg	Arg	Val	Leu	Tyr	Asn	Arg	Ala	Ser	Ala	Asp		
		770				775					780						
Ile	Asn	Gly	Lys	Pro	Trp	Asp	Pro	Lys	Arg	Met	Leu	Ile	Gln	Trp	Asn		
785					790					795					800		
Gly	Ser	Lys	Trp	Thr	Gly	Asn	Asp	Ile	Pro	Asp	Phe	Gly	Asn	Ala	Ala		
			805					810						815			
Pro	Gly	Thr	Pro	Thr	Gly	Pro	Phe	Ile	Met	Gln	Pro	Glu	Gly	Met	Gly		
			820				825						830				
Arg	Leu	Phe	Ala	Ile	Asn	Lys	Met	Ala	Glu	Gly	Pro	Phe	Pro	Glu	His		
		835				840						845					
Tyr	Glu	Pro	Ile	Glu	Thr	Pro	Leu	Gly	Thr	Asn	Pro	Leu	His	Pro	Asn		
		850				855					860						
Val	Val	Ser	Asn	Pro	Val	Val	Arg	Leu	Tyr	Glu	Gln	Asp	Ala	Leu	Arg		
865				870						875					880		
Met	Gly	Lys	Lys	Glu	Gln	Phe	Pro	Tyr	Val	Gly	Thr	Thr	Tyr	Arg	Leu		
			885					890						895			
Thr	Glu	His	Phe	His	Thr	Trp	Thr	Lys	His	Ala	Leu	Leu	Asn	Ala	Ile		
			900					905					910				
Ala	Gln	Pro	Glu	Gln	Phe	Val	Glu	Ile	Ser	Glu	Thr	Leu	Ala	Ala	Ala		
		915				920						925					
Lys	Gly	Ile	Asn	Asn	Gly	Asp	Arg	Val	Thr	Val	Ser	Ser	Lys	Arg	Gly		
		930				935					940						
Phe	Ile	Arg	Ala	Val	Ala	Val	Val	Thr	Arg	Arg	Leu	Lys	Pro	Leu	Asn		
945				950						955					960		
Val	Asn	Gly	Gln	Gln	Val	Glu	Thr	Val	Gly	Ile	Pro	Ile	His	Trp	Gly		
			965						970					975			
Phe	Glu	Gly	Val	Ala	Arg	Lys	Gly	Tyr	Ile	Ala	Asn	Thr	Leu	Thr	Pro		
			980				985						990				
Asn	Val	Gly	Asp	Ala	Asn	Ser	Gln	Thr	Pro	Glu	Tyr	Lys	Ala	Phe	Leu		
		995					1000					1005					
Val	Asn	Ile	Glu	Lys	Ala												
		1010															

<210> 267

<211> 294

<212> PRT

<213> E. Coli

<400> 267

Met	Ala	Met	Glu	Thr	Gln	Asp	Ile	Ile	Lys	Arg	Ser	Ala	Thr	Asn	Ser		
1				5					10					15			
Ile	Thr	Pro	Pro	Ser	Gln	Val	Arg	Asp	Tyr	Lys	Ala	Glu	Val	Ala	Lys		
			20					25					30				

Leu Ile Asp Val Ser Thr Cys Ile Gly Cys Lys Ala Cys Gln Val Ala
 35 40 45
 Cys Ser Glu Trp Asn Asp Ile Arg Asp Glu Val Gly His Cys Val Gly
 50 55 60
 Val Tyr Asp Asn Pro Ala Asp Leu Ser Ala Lys Ser Trp Thr Val Met
 65 70 75 80
 Arg Phe Ser Glu Thr Glu Gln Asn Gly Lys Leu Glu Trp Leu Ile Arg
 85 90 95
 Lys Asp Gly Cys Met His Cys Glu Asp Pro Gly Cys Leu Lys Ala Cys
 100 105 110
 Pro Ser Ala Gly Ala Ile Ile Gln Tyr Ala Asn Gly Ile Val Asp Phe
 115 120 125
 Gln Ser Glu Asn Cys Ile Gly Cys Gly Tyr Cys Ile Ala Gly Cys Pro
 130 135 140
 Phe Asn Ile Pro Arg Leu Asn Lys Glu Asp Asn Arg Val Tyr Lys Cys
 145 150 155 160
 Thr Leu Cys Val Asp Arg Val Ser Val Gly Gln Glu Pro Ala Cys Val
 165 170 175
 Lys Thr Cys Pro Thr Gly Ala Ile His Phe Gly Thr Lys Lys Glu Met
 180 185 190
 Leu Glu Leu Ala Glu Gln Arg Val Ala Lys Leu Lys Ala Arg Gly Tyr
 195 200 205
 Glu His Ala Gly Val Tyr Asn Pro Glu Gly Val Gly Gly Thr His Val
 210 215 220
 Met Tyr Val Leu His His Ala Asp Gln Pro Glu Leu Tyr His Gly Leu
 225 230 235 240
 Pro Lys Asp Pro Lys Ile Asp Thr Ser Val Ser Leu Trp Lys Gly Ala
 245 250 255
 Leu Lys Pro Leu Ala Ala Ala Gly Phe Ile Ala Thr Phe Ala Gly Leu
 260 265 270
 Ile Phe His Tyr Ile Gly Ile Gly Pro Asn Lys Glu Val Asp Asp Asp
 275 280 285
 Glu Glu Asp His His Glu
 290

<210> 268

<211> 217

<212> PRT

<213> E. Coli

<400> 268

Met Ser Lys Ser Lys Met Ile Val Arg Thr Lys Phe Ile Asp Arg Ala
 1 5 10 15
 Cys His Trp Thr Val Val Ile Cys Phe Phe Leu Val Ala Leu Ser Gly
 20 25 30
 Ile Ser Phe Phe Phe Pro Thr Leu Gln Trp Leu Thr Gln Thr Phe Gly
 35 40 45
 Thr Pro Gln Met Gly Arg Ile Leu His Pro Phe Phe Gly Ile Ala Ile
 50 55 60
 Phe Val Ala Leu Met Phe Met Phe Val Arg Phe Val His His Asn Ile
 65 70 75 80
 Pro Asp Lys Lys Asp Ile Pro Trp Leu Leu Asn Ile Val Glu Val Leu
 85 90 95
 Lys Gly Asn Glu His Lys Val Ala Asp Val Gly Lys Tyr Asn Ala Gly
 100 105 110
 Gln Lys Met Met Phe Trp Ser Ile Met Ser Met Ile Phe Val Leu Leu

		115					120					125					
Val	Thr	Gly	Val	Ile	Ile	Trp	Arg	Pro	Tyr	Phe	Ala	Gln	Tyr	Phe	Pro		
	130					135					140						
Met	Gln	Val	Val	Arg	Tyr	Ser	Leu	Leu	Ile	His	Ala	Ala	Ala	Gly	Ile		
145					150					155					160		
Ile	Leu	Ile	His	Ala	Ile	Leu	Ile	His	Met	Tyr	Met	Ala	Phe	Trp	Val		
				165					170					175			
Lys	Gly	Ser	Ile	Lys	Gly	Met	Ile	Glu	Gly	Lys	Val	Ser	Arg	Arg	Trp		
			180					185					190				
Ala	Lys	Lys	His	His	Pro	Arg	Trp	Tyr	Arg	Glu	Ile	Glu	Lys	Ala	Glu		
		195					200					205					
Ala	Lys	Lys	Glu	Ser	Glu	Glu	Gly	Ile									
	210					215											

<210> 269
 <211> 86
 <212> PRT
 <213> E. Coli

Met	Ala	Leu	Leu	Ile	Thr	Lys	Lys	Cys	Ile	Asn	Cys	Asp	Met	Cys	Glu		
1				5					10					15			
Pro	Glu	Cys	Pro	Asn	Glu	Ala	Ile	Ser	Met	Gly	Asp	His	Ile	Tyr	Glu		
			20					25					30				
Ile	Asn	Ser	Asp	Lys	Cys	Thr	Glu	Cys	Val	Gly	His	Tyr	Glu	Thr	Pro		
		35				40						45					
Thr	Cys	Gln	Lys	Val	Cys	Pro	Ile	Pro	Asn	Thr	Ile	Val	Lys	Asp	Pro		
	50				55						60						
Ala	His	Val	Glu	Thr	Glu	Gln	Leu	Trp	Asp	Lys	Phe	Val	Leu	Met			
65					70				75					80			
His	His	Ala	Asp	Lys	Ile												
				85													

<210> 270
 <211> 400
 <212> PRT
 <213> E. Coli

Met	Gln	Ser	Val	Asp	Val	Ala	Ile	Val	Gly	Gly	Gly	Met	Val	Gly	Leu		
1				5					10					15			
Ala	Val	Ala	Cys	Gly	Leu	Gln	Gly	Ser	Gly	Leu	Arg	Val	Ala	Val	Leu		
			20					25					30				
Glu	Gln	Arg	Val	Gln	Glu	Pro	Leu	Ala	Ala	Asn	Ala	Pro	Pro	Gln	Leu		
		35				40						45					
Arg	Val	Ser	Ala	Ile	Asn	Ala	Ala	Ser	Glu	Lys	Leu	Leu	Thr	Arg	Leu		
	50				55						60						
Gly	Val	Trp	Gln	Asp	Ile	Leu	Ser	Arg	Arg	Ala	Ser	Cys	Tyr	His	Gly		
65				70					75					80			
Met	Glu	Val	Trp	Asp	Lys	Asp	Ser	Phe	Gly	His	Ile	Ser	Phe	Asp	Asp		
				85					90					95			
Gln	Ser	Met	Gly	Tyr	Ser	His	Leu	Gly	His	Ile	Val	Glu	Asn	Ser	Val		
			100					105					110				
Ile	His	Tyr	Ala	Leu	Trp	Asn	Lys	Ala	His	Gln	Ser	Ser	Asp	Ile	Thr		
		115					120										

1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 23 24 25 26 27 28 29 30 31 32 33 34 35 36 37 38 39 40 41 42 43 44 45 46 47 48 49 50 51 52 53 54 55 56 57 58 59 60 61 62 63 64 65 66 67 68 69 70 71 72 73 74 75 76 77 78 79 80 81 82 83 84 85 86 87 88 89 90 91 92 93 94 95 96 97 98 99 100

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Leu Leu Ala Pro Ala Glu Leu Gln Gln Val Ala Trp Gly Glu Asn Glu
130      135      140
Thr Phe Leu Thr Leu Lys Asp Gly Ser Met Leu Thr Ala Arg Leu Val
145      150      155      160
Ile Gly Ala Asp Gly Ala Asn Ser Trp Leu Arg Asn Lys Ala Asp Ile
      165      170      175
Pro Leu Thr Phe Trp Asp Tyr Gln His His Ala Leu Val Ala Thr Ile
      180      185      190
Arg Thr Glu Glu Pro His Asp Ala Val Ala Arg Gln Val Phe His Gly
      195      200      205
Glu Gly Ile Leu Ala Phe Leu Pro Leu Ser Asp Pro His Leu Cys Ser
      210      215      220
Ile Val Trp Ser Leu Ser Pro Glu Glu Ala Gln Arg Met Gln Gln Ala
225      230      235      240
Ser Glu Asp Glu Phe Asn Arg Ala Leu Asn Ile Ala Phe Asp Asn Arg
      245      250      255
Leu Gly Leu Cys Lys Val Glu Ser Ala Arg Gln Val Phe Pro Leu Thr
      260      265      270
Gly Arg Tyr Ala Arg Gln Phe Ala Ser His Arg Leu Ala Leu Val Gly
      275      280      285
Asp Ala Ala His Thr Ile His Pro Leu Ala Gly Gln Gly Val Asn Leu
      290      295      300
Gly Phe Met Asp Ala Ala Glu Leu Ile Ala Glu Leu Lys Arg Leu His
305      310      315      320
Arg Gln Gly Lys Asp Ile Gly Gln Tyr Ile Tyr Leu Arg Arg Tyr Glu
      325      330      335
Arg Ser Arg Lys His Ser Ala Ala Leu Met Leu Ala Gly Met Gln Gly
      340      345      350
Phe Arg Asp Leu Phe Ser Gly Thr Asn Pro Ala Lys Lys Leu Leu Arg
      355      360      365
Asp Ile Gly Leu Lys Leu Ala Asp Thr Leu Pro Gly Val Lys Pro Gln
      370      375      380
Leu Ile Arg Gln Ala Met Gly Leu Asn Asp Leu Pro Glu Trp Leu Arg
385      390      395      400

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<210> 271
 <211> 392
 <212> PRT
 <213> E. Coli

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      <400> 271
Met Ser Val Ile Ile Val Gly Gly Gly Met Ala Gly Ala Thr Leu Ala
1      5      10      15
Leu Ala Ile Ser Arg Leu Ser His Gly Ala Leu Pro Val His Leu Ile
      20      25      30
Glu Ala Thr Ala Pro Glu Ser His Ala His Pro Gly Phe Asp Gly Arg
      35      40      45
Ala Ile Ala Leu Ala Ala Gly Thr Cys Gln Gln Leu Ala Arg Ile Gly
      50      55      60
Val Trp Gln Ser Leu Ala Asp Cys Ala Thr Ala Ile Thr Thr Val His
      65      70      75      80
Val Ser Asp Arg Gly His Ala Gly Phe Val Thr Leu Ala Ala Glu Asp
      85      90      95
Tyr Gln Leu Ala Ala Leu Gly Gln Val Val Glu Leu His Asn Val Gly
      100      105      110
Gln Arg Leu Phe Ala Leu Leu Arg Lys Ala Pro Gly Val Thr Leu His

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115 120 125
 130 135 140
 145 150 155 160
 165 170 175
 180 185 190
 195 200 205
 210 215 220
 225 230 235 240
 245 250 255
 260 265 270
 275 280 285
 290 295 300
 305 310 315 320
 325 330 335
 340 345 350
 355 360 365
 370 375 380
 385 390

Cys	Pro	Asp	Arg	Val	Ala	Asn	Val	Ala	Arg	Thr	Gln	Ser	His	Val	Glu
Val	Thr	Leu	Glu	Ser	Gly	Glu	Thr	Leu	Thr	Gly	Arg	Val	Leu	Val	Ala
Ala	Asp	Gly	Thr	His	Ser	Ala	Leu	Ala	Thr	Ala	Cys	Gly	Val	Asp	Trp
Gln	Gln	Glu	Pro	Tyr	Glu	Gln	Leu	Ala	Val	Ile	Ala	Asn	Val	Ala	Thr
Ser	Val	Ala	His	Glu	Gly	Arg	Ala	Phe	Glu	Arg	Phe	Thr	Gln	His	Gly
Pro	Leu	Ala	Met	Leu	Pro	Met	Ser	Asp	Gly	Arg	Cys	Ser	Leu	Val	Trp
Cys	His	Pro	Leu	Glu	Arg	Arg	Glu	Glu	Val	Leu	Ser	Trp	Ser	Asp	Glu
Lys	Phe	Cys	Arg	Glu	Leu	Gln	Ser	Ala	Phe	Gly	Trp	Arg	Leu	Gly	Lys
Ile	Thr	His	Ala	Gly	Lys	Arg	Ser	Ala	Tyr	Pro	Leu	Ala	Leu	Thr	His
Ala	Ala	Arg	Ser	Ile	Thr	His	Arg	Thr	Val	Leu	Val	Gly	Asn	Ala	Ala
Gln	Thr	Leu	His	Pro	Ile	Ala	Gly	Gln	Gly	Phe	Asn	Leu	Gly	Met	Arg
Asp	Val	Met	Ser	Leu	Ala	Glu	Thr	Leu	Thr	Gln	Ala	Gln	Glu	Arg	Gly
Glu	Asp	Met	Gly	Asp	Tyr	Gly	Val	Leu	Cys	Arg	Tyr	Gln	Gln	Arg	Arg
Gln	Ser	Asp	Arg	Glu	Ala	Thr	Ile	Gly	Val	Thr	Asp	Ser	Leu	Val	His
Leu	Phe	Ala	Asn	Arg	Trp	Ala	Pro	Leu	Val	Val	Gly	Arg	Asn	Ile	Gly
Leu	Met	Thr	Met	Glu	Leu	Phe	Thr	Pro	Ala	Arg	Asp	Val	Leu	Ala	Gln
Arg	Thr	Leu	Gly	Trp	Val	Ala	Arg								

<210> 272
 <211> 441
 <212> PRT
 <213> E. Coli

Met	Ser	Glu	Ile	Ser	Arg	Gln	Glu	Phe	Gln	Arg	Arg	Arg	Gln	Ala	Leu
Val	Glu	Gln	Met	Gln	Pro	Gly	Ser	Ala	Ala	Leu	Ile	Phe	Ala	Ala	Pro
Glu	Val	Thr	Arg	Ser	Ala	Asp	Ser	Glu	Tyr	Pro	Tyr	Arg	Gln	Asn	Ser
Asp	Phe	Trp	Tyr	Phe	Thr	Gly	Phe	Asn	Glu	Pro	Glu	Ala	Val	Leu	Val
Leu	Ile	Lys	Ser	Asp	Asp	Thr	His	Asn	His	Ser	Val	Leu	Phe	Asn	Arg
Val	Arg	Asp	Leu	Thr	Ala	Glu	Ile	Trp	Phe	Gly	Arg	Arg	Leu	Gly	Gln
Asp	Ala	Ala	Pro	Glu	Lys	Leu	Gly	Val	Asp	Arg	Ala	Leu	Ala	Phe	Ser

50		55		60
Glu Leu Ala Gln Ala Leu Arg Lys Met His Ser Ala Thr Ser Asp Ala				
65		70		80
Leu Gln Asp Asp Gly Phe Leu Phe Gln Leu Tyr Leu Pro Asp Gly Asp				
	85		90	95
Asp Val Ser Val Phe Asp Arg Ala Asp Ala Leu Ala Gly Trp Val Asn				
	100		105	110
His Phe Leu Leu Gly Leu Gly Val Thr Gln Pro Lys Leu Asp Lys Val				
	115		120	125
Thr Gly Glu Thr Gly Glu Ala Ile Asp Asp Leu Arg Asn Ile Ala Gln				
	130		135	140
Leu Gly Tyr Asp Glu Asp Glu Asp Gln Glu Glu Leu Glu Met Ser Leu				
145		150		160
Glu Glu Ile Ile Glu Tyr Val Arg Val Ala Ala Leu Leu Cys His Asp				
	165		170	175
Thr Phe Thr His Pro Gln Pro Thr Ala Pro Glu Val Gln Lys Pro Thr				
	180		185	190
Leu His				

<210> 274
 <211> 120
 <212> PRT
 <213> E. Coli

<400> 274
Met Leu Lys Leu Phe Ala Lys Tyr Thr Ser Ile Gly Val Leu Asn Thr
1 5 10 15
Leu Ile His Trp Val Val Phe Gly Val Cys Ile Tyr Val Ala His Thr
20 25 30
Asn Gln Ala Leu Ala Asn Phe Ala Gly Phe Val Val Ala Val Ser Phe
35 40 45
Ser Phe Phe Ala Asn Ala Lys Phe Thr Phe Lys Ala Ser Thr Thr Thr
50 55 60
Met Arg Tyr Met Leu Tyr Val Gly Phe Met Gly Thr Leu Ser Ala Thr
65 70 75 80
Val Gly Trp Ala Ala Asp Arg Cys Ala Leu Pro Pro Met Ile Thr Leu
85 90 95
Val Thr Phe Ser Ala Ile Ser Leu Val Cys Gly Phe Val Tyr Ser Lys
100 105 110
Phe Ile Val Phe Arg Asp Ala Lys
115 120

<210> 275
 <211> 306
 <212> PRT
 <213> E. Coli

<400> 275
Met Lys Ile Ser Leu Val Val Pro Val Phe Asn Glu Glu Glu Ala Ile
1 5 10 15
Pro Ile Phe Tyr Lys Thr Val Arg Glu Phe Glu Glu Leu Lys Ser Tyr
20 25 30
Glu Val Glu Ile Val Phe Ile Asn Asp Gly Ser Lys Asp Ala Thr Glu
35 40 45
Ser Ile Ile Asn Ala Leu Ala Val Ser Asp Pro Leu Val Val Pro Leu

50 55 60
 Ser Phe Thr Arg Asn Phe Gly Lys Glu Pro Ala Leu Phe Ala Gly Leu
 65 70 75 80
 Asp His Ala Thr Gly Asp Ala Ile Ile Pro Ile Asp Val Asp Leu Gln
 85 90 95
 Asp Pro Ile Glu Val Ile Pro His Leu Ile Glu Lys Trp Gln Ala Gly
 100 105 110
 Ala Asp Met Val Leu Ala Lys Arg Ser Asp Arg Ser Thr Asp Gly Arg
 115 120 125
 Leu Lys Arg Lys Thr Ala Glu Trp Phe Tyr Lys Leu His Asn Lys Ile
 130 135 140
 Ser Asn Pro Lys Ile Glu Asn Val Gly Asp Phe Arg Leu Met Ser
 145 150 155 160
 Arg Asp Val Val Glu Asn Ile Lys Leu Met Pro Glu Arg Asn Leu Phe
 165 170 175
 Met Lys Gly Ile Leu Ser Trp Val Gly Gly Lys Thr Asp Ile Val Glu
 180 185 190
 Tyr Val Arg Ala Glu Arg Ile Ala Gly Asp Thr Lys Phe Asn Gly Trp
 195 200 205
 Lys Leu Trp Asn Leu Ala Leu Glu Gly Ile Thr Ser Phe Ser Thr Phe
 210 215 220
 Pro Leu Arg Ile Trp Thr Tyr Ile Gly Leu Val Val Ala Ser Val Ala
 225 230 235 240
 Phe Ile Tyr Gly Ala Trp Met Ile Leu Asp Thr Ile Ile Phe Gly Asn
 245 250 255
 Ala Val Arg Gly Tyr Pro Ser Leu Leu Val Ser Ile Leu Phe Leu Gly
 260 265 270
 Gly Ile Gln Met Ile Gly Ile Gly Val Leu Gly Glu Tyr Ile Gly Arg
 275 280 285
 Thr Tyr Ile Glu Thr Lys Lys Arg Pro Lys Tyr Ile Ile Lys Arg Val
 290 295 300
 Lys Lys
 305

<210> 276
 <211> 443
 <212> PRT
 <213> E. Coli

<400> 276
 Met Asn Lys Ala Ile Lys Val Ser Leu Tyr Ile Ser Phe Val Leu Ile
 1 5 10 15
 Ile Cys Ala Leu Ser Lys Asn Ile Met Met Leu Asn Thr Ser Asp Phe
 20 25 30
 Gly Arg Ala Ile Lys Pro Leu Ile Glu Asp Ile Pro Ala Phe Thr Tyr
 35 40 45
 Asp Leu Pro Leu Leu Tyr Lys Leu Lys Gly His Ile Asp Ser Ile Asp
 50 55 60
 Ser Tyr Glu Tyr Ile Ser Ser Tyr Ser Tyr Ile Leu Tyr Thr Tyr Val
 65 70 75 80
 Leu Phe Ile Ser Ile Phe Thr Glu Tyr Leu Asp Ala Arg Val Leu Ser
 85 90 95
 Leu Phe Leu Lys Val Ile Tyr Ile Tyr Ser Leu Tyr Ala Ile Phe Thr
 100 105 110
 Ser Tyr Ile Lys Thr Glu Arg Tyr Val Thr Leu Phe Thr Phe Phe Ile
 115 120 125

Leu Ala Phe Leu Met Cys Ser Ser Ser Thr Leu Ser Met Phe Ala Ser
 130 135 140
 Phe Tyr Gln Glu Gln Ile Val Ile Ile Phe Leu Pro Phe Leu Val Tyr
 145 150 155 160
 Ser Leu Thr Cys Lys Asn Asn Lys Ser Met Leu Leu Leu Phe Phe Ser
 165 170 175
 Leu Leu Ile Ile Ser Thr Ala Lys Asn Gln Phe Ile Leu Thr Pro Leu
 180 185 190
 Ile Val Tyr Ser Tyr Tyr Ile Phe Phe Asp Arg His Lys Leu Ile Ile
 195 200 205
 Lys Ser Val Ile Cys Val Val Cys Leu Leu Ala Ser Ile Phe Ala Ile
 210 215 220
 Ser Tyr Ser Lys Gly Val Val Glu Leu Asn Lys Tyr His Ala Thr Tyr
 225 230 235 240
 Phe Gly Ser Tyr Leu Tyr Met Lys Asn Asn Gly Tyr Lys Met Pro Ser
 245 250 255
 Tyr Val Asp Asp Lys Cys Val Gly Leu Asp Ala Trp Gly Asn Lys Phe
 260 265 270
 Asp Ile Ser Phe Gly Ala Thr Pro Thr Glu Val Gly Thr Glu Cys Phe
 275 280 285
 Glu Ser His Lys Asp Glu Thr Phe Ser Asn Ala Leu Phe Leu Leu Val
 290 295 300
 Ser Lys Pro Ser Thr Ile Phe Lys Leu Pro Phe Asp Asp Gly Val Met
 305 310 315 320
 Ser Gln Tyr Lys Glu Asn Tyr Phe His Val Tyr Lys Lys Leu His Val
 325 330 335
 Ile Tyr Gly Glu Ser Asn Ile Leu Thr Thr Ile Thr Asn Ile Lys Asp
 340 345 350
 Asn Ile Phe Lys Asn Ile Arg Phe Ile Ser Leu Leu Leu Phe Phe Ile
 355 360 365
 Ala Ser Ile Phe Ile Arg Asn Asn Lys Ile Lys Ala Ser Leu Phe Val
 370 375 380
 Val Ser Leu Phe Gly Ile Ser Gln Phe Tyr Val Ser Phe Phe Gly Glu
 385 390 395 400
 Gly Tyr Arg Asp Leu Ser Lys His Leu Phe Gly Met Tyr Phe Ser Phe
 405 410 415
 Asp Leu Cys Leu Tyr Ile Thr Val Val Phe Leu Ile Tyr Lys Ile Ile
 420 425 430
 Gln Arg Asn Gln Asp Asn Ser Asp Val Lys His
 435 440

<210> 277
 <211> 82
 <212> PRT
 <213> E. Coli

<400> 277
 Met Gly Ile Leu Ser Trp Ile Ile Phe Gly Leu Ile Ala Gly Ile Leu
 1 5 10 15
 Ala Lys Trp Ile Met Pro Gly Lys Asp Gly Gly Gly Phe Phe Met Thr
 20 25 30
 Ile Leu Leu Gly Ile Val Gly Ala Val Val Gly Gly Trp Ile Ser Thr
 35 40 45
 Leu Phe Gly Phe Gly Lys Val Asp Gly Phe Asn Phe Gly Ser Phe Val
 50 55 60

Val Ala Val Ile Gly Ala Ile Val Val Leu Phe Ile Tyr Arg Lys Ile
 65 70 75 80
 Lys Ser

<210> 278
 <211> 60
 <212> PRT
 <213> E. Coli

<400> 278
 Met Gly Lys Ala Thr Tyr Thr Val Thr Val Thr Asn Asn Ser Asn Gly
 1 5 10 15
 Val Ser Val Asp Tyr Glu Thr Glu Thr Pro Met Thr Leu Leu Val Pro
 20 25 30
 Glu Val Ala Ala Glu Val Ile Lys Asp Leu Val Asn Thr Val Arg Ser
 35 40 45
 Tyr Asp Thr Glu Asn Glu His Asp Val Cys Gly Trp
 50 55 60

<210> 279
 <211> 119
 <212> PRT
 <213> E. Coli

<400> 279
 Met Leu Gln Ile Pro Gln Asn Tyr Ile His Thr Arg Ser Thr Pro Phe
 1 5 10 15
 Trp Asn Lys Gln Thr Ala Pro Ala Gly Ile Phe Glu Arg His Leu Asp
 20 25 30
 Lys Gly Thr Arg Pro Gly Val Tyr Pro Arg Leu Ser Val Met His Gly
 35 40 45
 Ala Val Lys Tyr Leu Gly Tyr Ala Asp Glu His Ser Ala Glu Pro Asp
 50 55 60
 Gln Val Ile Leu Ile Glu Ala Gly Gln Phe Ala Val Phe Pro Pro Glu
 65 70 75 80
 Lys Trp His Asn Ile Glu Ala Met Thr Asp Asp Thr Tyr Phe Asn Ile
 85 90 95
 Asp Phe Phe Val Ala Pro Glu Val Leu Met Glu Gly Ala Gln Gln Arg
 100 105 110
 Lys Val Ile His Asn Gly Lys
 115

<210> 280
 <211> 246
 <212> PRT
 <213> E. Coli

<400> 280
 Met Lys Phe Lys Val Ile Ala Leu Ala Ala Leu Met Gly Ile Ser Gly
 1 5 10 15
 Met Ala Ala Gln Ala Asn Glu Leu Pro Asp Gly Pro His Ile Val Thr
 20 25 30
 Ser Gly Thr Ala Ser Val Asp Ala Val Pro Asp Ile Ala Thr Leu Ala

Ala	Gln	Ala	Gln	Gly	Gln	Leu	Ala	Lys	Asp	Lys	Ala	Thr	Leu	Ala	Asn
			180					185					190		
Ala	Arg	Arg	Asp	Leu	Ala	Arg	Tyr	Gln	Gln	Leu	Ala	Lys	Thr	Asn	Leu
			195				200					205			
Val	Ser	Arg	Gln	Glu	Leu	Asp	Ala	Gln	Gln	Ala	Leu	Val	Ser	Glu	Thr
			210			215					220				
Glu	Gly	Thr	Ile	Lys	Ala	Asp	Glu	Ala	Ser	Val	Ala	Ser	Ala	Gln	Leu
225					230					235					240
Gln	Leu	Asp	Trp	Ser	Arg	Ile	Thr	Ala	Pro	Val	Asp	Gly	Arg	Val	Gly
				245					250					255	
Leu	Lys	Gln	Val	Asp	Val	Gly	Asn	Gln	Ile	Ser	Ser	Gly	Asp	Thr	Thr
			260				265						270		
Gly	Ile	Val	Val	Ile	Thr	Gln	Thr	His	Pro	Ile	Asp	Leu	Val	Phe	Thr
			275				280					285			
Leu	Pro	Glu	Ser	Asp	Ile	Ala	Thr	Val	Val	Gln	Ala	Gln	Lys	Ala	Gly
			290			295					300				
Lys	Pro	Leu	Val	Val	Glu	Ala	Trp	Asp	Arg	Thr	Asn	Ser	Lys	Lys	Leu
305					310					315					320
Ser	Glu	Gly	Thr	Leu	Leu	Ser	Leu	Asp	Asn	Gln	Ile	Asp	Ala	Thr	Thr
				325					330					335	
Gly	Thr	Ile	Lys	Val	Lys	Ala	Arg	Phe	Asn	Asn	Gln	Asp	Asp	Ala	Leu
			340					345					350		
Phe	Pro	Asn	Gln	Phe	Val	Asn	Ala	Arg	Met	Leu	Val	Asp	Thr	Glu	Gln
			355				360					365			
Asn	Ala	Val	Val	Ile	Pro	Thr	Ala	Ala	Leu	Gln	Met	Gly	Asn	Glu	Gly
			370			375					380				
His	Phe	Val	Trp	Val	Leu	Asn	Ser	Glu	Asn	Lys	Val	Ser	Lys	His	Leu
385					390					395					400
Val	Thr	Pro	Gly	Ile	Gln	Asp	Ser	Gln	Lys	Val	Val	Ile	Arg	Ala	Gly
				405					410					415	
Ile	Ser	Ala	Gly	Asp	Arg	Val	Val	Thr	Asp	Gly	Ile	Asp	Arg	Leu	Thr
			420					425				430			
Glu	Gly	Ala	Lys	Val	Glu	Val	Val	Glu	Ala	Gln	Ser	Ala	Thr	Thr	Pro
			435				440					445			
Glu	Glu	Lys	Ala	Thr	Ser	Arg	Glu	Tyr	Ala	Lys	Lys	Gly	Ala	Arg	Ser
			450			455					460				

<210> 282
 <211> 1040
 <212> PRT
 <213> E. Coli

<400> 282															
Met	Gln	Val	Leu	Pro	Pro	Ser	Ser	Thr	Gly	Gly	Pro	Ser	Arg	Leu	Phe
1				5					10					15	
Ile	Met	Arg	Pro	Val	Ala	Thr	Thr	Leu	Leu	Met	Val	Ala	Ile	Leu	Leu
			20					25					30		
Ala	Gly	Ile	Ile	Gly	Tyr	Arg	Ala	Leu	Pro	Val	Ser	Ala	Leu	Pro	Glu
			35				40					45			
Val	Asp	Tyr	Pro	Thr	Ile	Gln	Val	Val	Thr	Leu	Tyr	Pro	Gly	Ala	Ser
	50					55					60				
Pro	Asp	Val	Met	Thr	Ser	Ala	Val	Thr	Ala	Pro	Leu	Glu	Arg	Gln	Phe
65					70					75					80
Gly	Gln	Met	Ser	Gly	Leu	Lys	Gln	Met	Ser	Ser	Gln	Ser	Ser	Gly	Gly
				85					90					95	
Ala	Ser	Val	Ile	Thr	Leu	Gln	Phe	Gln	Leu	Thr	Leu	Pro	Leu	Asp	Val

Phe	Phe	Pro	Val	Gln	Asp	Asn	Gly	Ile	Ile	Gln	Gly	Thr	Leu	Gln	Ala	
				565					570					575		
Pro	Gln	Ser	Ser	Ser	Phe	Ala	Asn	Met	Ala	Gln	Arg	Gln	Arg	Gln	Val	
				580				585						590		
Ala	Asp	Val	Ile	Leu	Gln	Asp	Pro	Ala	Val	Gln	Ser	Leu	Thr	Ser	Phe	
				595			600					605				
Val	Gly	Val	Asp	Gly	Thr	Asn	Pro	Ser	Leu	Asn	Ser	Ala	Arg	Leu	Gln	
	610					615					620					
Ile	Asn	Leu	Lys	Pro	Leu	Asp	Glu	Arg	Asp	Asp	Arg	Val	Gln	Lys	Val	
625					630					635					640	
Ile	Ala	Arg	Leu	Gln	Thr	Ala	Val	Asp	Lys	Val	Pro	Gly	Val	Asp	Leu	
				645					650					655		
Phe	Leu	Gln	Pro	Thr	Gln	Asp	Leu	Thr	Ile	Asp	Thr	Gln	Val	Ser	Arg	
			660					665					670			
Thr	Gln	Tyr	Gln	Phe	Thr	Leu	Gln	Ala	Thr	Ser	Leu	Asp	Ala	Leu	Ser	
		675					680					685				
Thr	Trp	Val	Pro	Gln	Leu	Met	Glu	Lys	Leu	Gln	Gln	Leu	Pro	Gln	Leu	
	690					695					700					
Ser	Asp	Val	Ser	Ser	Asp	Trp	Gln	Asp	Lys	Gly	Leu	Val	Ala	Tyr	Val	
705					710					715					720	
Asn	Val	Asp	Arg	Asp	Ser	Ala	Ser	Arg	Leu	Gly	Ile	Ser	Met	Ala	Asp	
				725					730					735		
Val	Asp	Asn	Ala	Leu	Tyr	Asn	Ala	Phe	Gly	Gln	Arg	Leu	Ile	Ser	Thr	
			740					745					750			
Ile	Tyr	Thr	Gln	Ala	Asn	Gln	Tyr	Arg	Val	Val	Leu	Glu	His	Asn	Thr	
	755						760					765				
Glu	Asn	Thr	Pro	Gly	Leu	Ala	Ala	Leu	Asp	Thr	Ile	Arg	Leu	Thr	Ser	
	770					775					780					
Ser	Asp	Gly	Gly	Val	Val	Pro	Leu	Ser	Ser	Ile	Ala	Lys	Ile	Glu	Gln	
785					790					795					800	
Arg	Phe	Ala	Pro	Leu	Ser	Ile	Asn	His	Leu	Asp	Gln	Phe	Pro	Val	Thr	
			805						810					815		
Thr	Ile	Ser	Phe	Asn	Val	Pro	Asp	Asn	Tyr	Ser	Leu	Gly	Asp	Ala	Val	
			820					825					830			
Gln	Ala	Ile	Met	Asp	Thr	Glu	Lys	Thr	Leu	Asn	Leu	Pro	Val	Asp	Ile	
		835					840					845				
Thr	Thr	Gln	Phe	Gln	Gly	Ser	Thr	Leu	Ala	Phe	Gln	Ser	Ala	Leu	Gly	
	850					855					860					
Ser	Thr	Val	Trp	Leu	Ile	Val	Ala	Ala	Val	Val	Ala	Met	Tyr	Ile	Val	
865					870					875					880	
Leu	Gly	Ile	Leu	Tyr	Glu	Ser	Phe	Ile	His	Pro	Ile	Thr	Ile	Leu	Ser	
				885					890					895		
Thr	Leu	Pro	Thr	Ala	Gly	Val	Gly	Ala	Leu	Leu	Ala	Leu	Leu	Ile	Ala	
			900					905					910			
Gly	Ser	Glu	Leu	Asp	Val	Ile	Ala	Ile	Ile	Gly	Ile	Ile	Leu	Leu	Ile	
		915					920					925				
Gly	Ile	Val	Lys	Lys	Asn	Ala	Ile	Met	Met	Ile	Asp	Phe	Ala	Leu	Ala	
	930					935					940					
Ala	Glu	Arg	Glu	Gln	Gly	Met	Ser	Pro	Arg	Glu	Ala	Ile	Tyr	Gln	Ala	
945					950					955					960	
Cys	Leu	Leu	Arg	Phe	Arg	Pro	Ile	Leu	Met	Thr	Thr	Leu	Ala	Ala	Leu	
				965					970					975		
Leu	Gly	Ala	Leu	Pro	Leu	Met	Leu	Ser	Thr	Gly	Val	Gly	Ala	Glu	Leu	
			980					985					990			
Arg	Arg	Pro	Leu	Gly	Ile	Gly	Met	Val	Gly	Gly	Leu	Ile	Val	Ser	Gln	
		995					1000					1005				
Val	Leu	Thr	Leu	Phe	Thr	Thr	Pro	Val	Ile	Tyr	Leu	Leu	Phe	Asp	Arg	

1010		1015		1020
Leu Ala Leu Trp Thr	Lys Ser Arg Phe Ala	Arg His Glu Glu Glu Ala		
1025	1030	1035		1040

<210> 283
 <211> 1025
 <212> PRT
 <213> E. Coli

<400> 283

Met	Lys	Phe	Phe	Ala	Leu	Phe	Ile	Tyr	Arg	Pro	Val	Ala	Thr	Ile	Leu
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Leu	Ser	Val	Ala	Ile	Thr	Leu	Cys	Gly	Ile	Leu	Gly	Phe	Arg	Met	Leu
			20					25					30		
Pro	Val	Ala	Pro	Leu	Pro	Gln	Val	Asp	Phe	Pro	Val	Ile	Ile	Val	Ser
		35					40					45			
Ala	Ser	Leu	Pro	Gly	Ala	Ser	Pro	Glu	Thr	Met	Ala	Ser	Ser	Val	Ala
	50					55					60				
Thr	Pro	Leu	Glu	Arg	Ser	Leu	Gly	Arg	Ile	Ala	Gly	Val	Ser	Glu	Met
65					70					75					80
Thr	Ser	Ser	Ser	Ser	Leu	Gly	Ser	Thr	Arg	Ile	Ile	Leu	Gln	Phe	Asp
				85					90					95	
Phe	Asp	Arg	Asp	Ile	Asn	Gly	Ala	Ala	Arg	Asp	Val	Gln	Ala	Ala	Ile
			100				105						110		
Asn	Ala	Ala	Gln	Ser	Leu	Leu	Pro	Ser	Gly	Met	Pro	Ser	Arg	Pro	Thr
	115						120					125			
Tyr	Arg	Lys	Ala	Asn	Pro	Ser	Asp	Ala	Pro	Ile	Met	Ile	Leu	Thr	Leu
	130					135					140				
Thr	Ser	Asp	Thr	Tyr	Ser	Gln	Gly	Glu	Leu	Tyr	Asp	Phe	Ala	Ser	Thr
145					150					155					160
Gln	Leu	Ala	Pro	Thr	Ile	Ser	Gln	Ile	Asp	Gly	Val	Gly	Asp	Val	Asp
				165					170					175	
Val	Gly	Gly	Ser	Ser	Leu	Pro	Ala	Val	Arg	Val	Gly	Leu	Asn	Pro	Gln
			180					185					190		
Ala	Leu	Phe	Asn	Gln	Gly	Val	Ser	Leu	Asp	Asp	Val	Arg	Thr	Ala	Val
		195					200					205			
Ser	Asn	Ala	Asn	Val	Arg	Lys	Pro	Gln	Gly	Ala	Leu	Glu	Asp	Gly	Thr
	210					215					220				
His	Arg	Trp	Gln	Ile	Gln	Thr	Asn	Asp	Glu	Leu	Lys	Thr	Ala	Ala	Glu
225					230					235					240
Tyr	Gln	Pro	Leu	Ile	Ile	His	Tyr	Asn	Asn	Gly	Gly	Ala	Val	Arg	Leu
				245					250					255	
Gly	Asp	Val	Ala	Thr	Val	Thr	Asp	Ser	Val	Gln	Asp	Val	Arg	Asn	Ala
			260				265						270		
Gly	Met	Thr	Asn	Ala	Lys	Pro	Ala	Ile	Leu	Leu	Met	Ile	Arg	Lys	Leu
		275					280					285			
Pro	Glu	Ala	Asn	Ile	Ile	Gln	Thr	Val	Asp	Ser	Ile	Arg	Ala	Lys	Leu
	290					295					300				
Pro	Glu	Leu	Gln	Glu	Thr	Ile	Pro	Ala	Ala	Ile	Asp	Leu	Gln	Ile	Ala
305					310					315					320
Gln	Asp	Arg	Ser	Pro	Thr	Ile	Arg	Ala	Ser	Leu	Glu	Glu	Val	Glu	Gln
				325					330					335	
Thr	Leu	Ile	Ile	Ser	Val	Ala	Leu	Val	Ile	Leu	Val	Val	Phe	Leu	Phe
			340				345						350		
Leu	Arg	Ser	Gly	Arg	Ala	Thr	Ile	Ile	Pro	Ala	Val	Ser	Val	Pro	Val
		355					360					365			

Ser	Leu	Ile	Gly	Thr	Phe	Ala	Ala	Met	Tyr	Leu	Cys	Gly	Phe	Ser	Leu
370						375					380				
Asn	Asn	Leu	Ser	Leu	Met	Ala	Leu	Thr	Ile	Ala	Thr	Gly	Phe	Val	Val
385					390					395					400
Asp	Asp	Ala	Ile	Val	Val	Leu	Glu	Asn	Ile	Ala	Arg	His	Leu	Glu	Ala
				405					410					415	
Gly	Met	Lys	Pro	Leu	Gln	Ala	Ala	Leu	Gln	Gly	Thr	Arg	Glu	Val	Gly
			420					425					430		
Phe	Thr	Val	Leu	Ser	Met	Ser	Leu	Ser	Leu	Val	Ala	Val	Phe	Leu	Pro
		435					440					445			
Leu	Leu	Leu	Met	Gly	Gly	Leu	Pro	Gly	Arg	Leu	Leu	Arg	Glu	Phe	Ala
450						455					460				
Val	Thr	Leu	Ser	Val	Ala	Ile	Gly	Ile	Ser	Leu	Leu	Val	Ser	Leu	Thr
465					470					475					480
Leu	Thr	Pro	Met	Met	Cys	Gly	Trp	Met	Leu	Lys	Ala	Ser	Lys	Pro	Arg
				485					490					495	
Glu	Gln	Lys	Arg	Leu	Arg	Gly	Phe	Gly	Arg	Met	Leu	Val	Ala	Leu	Gln
			500					505					510		
Gln	Gly	Tyr	Gly	Lys	Ser	Leu	Lys	Trp	Val	Leu	Asn	His	Thr	Arg	Leu
		515					520					525			
Val	Gly	Val	Val	Leu	Leu	Gly	Thr	Ile	Ala	Leu	Asn	Ile	Trp	Leu	Tyr
530						535					540				
Ile	Ser	Ile	Pro	Lys	Thr	Phe	Phe	Pro	Glu	Gln	Asp	Thr	Gly	Val	Leu
545					550					555					560
Met	Gly	Gly	Ile	Gln	Ala	Asp	Gln	Ser	Ile	Ser	Phe	Gln	Ala	Met	Arg
				565					570					575	
Gly	Lys	Leu	Gln	Asp	Phe	Met	Lys	Ile	Ile	Arg	Asp	Asp	Pro	Ala	Val
			580				585						590		
Asp	Asn	Val	Thr	Gly	Phe	Thr	Gly	Gly	Ser	Arg	Val	Asn	Ser	Gly	Met
		595					600					605			
Met	Phe	Ile	Thr	Leu	Lys	Pro	Arg	Asp	Glu	Arg	Ser	Glu	Thr	Ala	Gln
610						615					620				
Gln	Ile	Ile	Asp	Arg	Leu	Arg	Val	Lys	Leu	Ala	Lys	Glu	Pro	Gly	Ala
625					630					635					640
Asn	Leu	Phe	Leu	Met	Ala	Val	Gln	Asp	Ile	Arg	Val	Gly	Gly	Arg	Gln
				645					650					655	
Ser	Asn	Ala	Ser	Tyr	Gln	Tyr	Thr	Leu	Leu	Ser	Asp	Asp	Leu	Ala	Ala
			660					665					670		
Leu	Arg	Glu	Trp	Glu	Pro	Lys	Ile	Arg	Lys	Lys	Leu	Ala	Thr	Leu	Pro
		675					680					685			
Glu	Leu	Ala	Asp	Val	Asn	Ser	Asp	Gln	Gln	Asp	Asn	Gly	Ala	Glu	Met
690					695						700				
Asn	Leu	Val	Tyr	Asp	Arg	Asp	Thr	Met	Ala	Arg	Leu	Gly	Ile	Asp	Val
705					710					715					720
Gln	Ala	Ala	Asn	Ser	Leu	Leu	Asn	Asn	Ala	Phe	Gly	Gln	Arg	Gln	Ile
			725						730					735	
Ser	Thr	Ile	Tyr	Gln	Pro	Met	Asn	Gln	Tyr	Lys	Val	Val	Met	Glu	Val
		740					745						750		
Asp	Pro	Arg	Tyr	Thr	Gln	Asp	Ile	Ser	Ala	Leu	Glu	Lys	Met	Phe	Val
		755					760					765			
Ile	Asn	Asn	Glu	Gly	Lys	Ala	Ile	Pro	Leu	Ser	Tyr	Phe	Ala	Lys	Trp
770					775						780				
Gln	Pro	Ala	Asn	Ala	Pro	Leu	Ser	Val	Asn	His	Gln	Gly	Leu	Ser	Ala
785					790					795					800
Ala	Ser	Thr	Ile	Ser	Phe	Asn	Leu	Pro	Thr	Gly	Lys	Ser	Leu	Ser	Asp
			805						810					815	
Ala	Ser	Ala	Ala	Ile	Asp	Arg	Ala	Met	Thr	Gln	Leu	Gly	Val	Pro	Ser

			820					825				830				
Thr	Val	Arg	Gly	Ser	Phe	Ala	Gly	Thr	Ala	Gln	Val	Phe	Gln	Glu	Thr	
		835					840					845				
Met	Asn	Ser	Gln	Val	Ile	Leu	Ile	Ile	Ala	Ala	Ile	Ala	Thr	Val	Tyr	
	850					855					860					
Ile	Val	Leu	Gly	Ile	Leu	Tyr	Glu	Ser	Tyr	Val	His	Pro	Leu	Thr	Ile	
865					870				875						880	
Leu	Ser	Thr	Leu	Pro	Ser	Ala	Gly	Val	Gly	Ala	Leu	Leu	Ala	Leu	Glu	
			885					890					895			
Leu	Phe	Asn	Ala	Pro	Phe	Ser	Leu	Ile	Ala	Leu	Ile	Gly	Ile	Met	Leu	
		900					905						910			
Leu	Ile	Gly	Ile	Val	Lys	Lys	Asn	Ala	Ile	Met	Met	Val	Asp	Phe	Ala	
	915						920					925				
Leu	Glu	Ala	Gln	Arg	His	Gly	Asn	Leu	Thr	Pro	Gln	Glu	Ala	Ile	Phe	
930						935					940					
Gln	Ala	Cys	Leu	Leu	Arg	Phe	Arg	Pro	Ile	Met	Met	Thr	Thr	Leu	Ala	
945					950					955					960	
Ala	Leu	Phe	Gly	Ala	Leu	Pro	Leu	Val	Leu	Ser	Gly	Gly	Asp	Gly	Ser	
			965					970						975		
Glu	Leu	Arg	Gln	Pro	Leu	Gly	Ile	Thr	Ile	Val	Gly	Gly	Leu	Val	Met	
			980					985					990			
Ser	Gln	Leu	Leu	Thr	Leu	Tyr	Thr	Thr	Pro	Val	Val	Tyr	Leu	Phe	Phe	
	995						1000					1005				
Asp	Arg	Leu	Arg	Leu	Arg	Phe	Ser	Arg	Lys	Pro	Lys	Gln	Thr	Val	Thr	
	1010					1015						1020				
Glu																
1025																

<210> 284

<211> 471

<212> PRT

<213> E. Coli

<400> 284

Met	Thr	Asp	Leu	Pro	Asp	Ser	Thr	Arg	Trp	Gln	Leu	Trp	Ile	Val	Ala	
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Phe	Gly	Phe	Phe	Met	Gln	Ser	Leu	Asp	Thr	Thr	Ile	Val	Asn	Thr	Ala	
			20					25					30			
Leu	Pro	Ser	Met	Ala	Gln	Ser	Leu	Gly	Glu	Ser	Pro	Leu	His	Met	His	
		35					40					45				
Met	Val	Ile	Val	Ser	Tyr	Val	Leu	Thr	Val	Ala	Val	Met	Leu	Pro	Ala	
	50					55					60					
Ser	Gly	Trp	Leu	Ala	Asp	Lys	Val	Gly	Val	Arg	Asn	Ile	Phe	Phe	Thr	
65					70					75					80	
Ala	Ile	Val	Leu	Phe	Thr	Leu	Gly	Ser	Leu	Phe	Cys	Ala	Leu	Ser	Gly	
			85					90					95			
Thr	Leu	Asn	Glu	Leu	Leu	Leu	Ala	Arg	Ala	Leu	Gln	Gly	Val	Gly	Gly	
		100						105					110			
Ala	Met	Met	Val	Pro	Val	Gly	Arg	Leu	Thr	Val	Met	Lys	Ile	Val	Pro	
		115					120					125				
Arg	Glu	Gln	Tyr	Met	Ala	Ala	Met	Thr	Phe	Val	Thr	Leu	Pro	Gly	Gln	
	130					135					140					
Val	Gly	Pro	Leu	Leu	Gly	Pro	Ala	Leu	Gly	Gly	Leu	Leu	Val	Glu	Tyr	
145					150					155					160	
Ala	Ser	Trp	His	Trp	Ile	Phe	Leu	Ile	Asn	Ile	Pro	Val	Gly	Ile	Ile	
				165					170					175		

Gly	Ala	Ile	Ala	Thr	Leu	Leu	Leu	Met	Pro	Asn	Tyr	Thr	Met	Gln	Thr
			180					185					190		
Arg	Arg	Phe	Asp	Leu	Ser	Gly	Phe	Leu	Leu	Leu	Ala	Val	Gly	Met	Ala
		195					200					205			
Val	Leu	Thr	Leu	Ala	Leu	Asp	Gly	Ser	Lys	Gly	Thr	Gly	Leu	Ser	Pro
	210					215					220				
Leu	Thr	Ile	Ala	Gly	Leu	Val	Ala	Val	Gly	Val	Val	Ala	Leu	Val	Leu
225					230					235					240
Tyr	Leu	Leu	His	Ala	Arg	Asn	Asn	Asn	Arg	Ala	Leu	Phe	Ser	Leu	Lys
			245						250					255	
Leu	Phe	Arg	Thr	Arg	Thr	Phe	Ser	Leu	Gly	Leu	Ala	Gly	Ser	Phe	Ala
			260					265					270		
Gly	Arg	Ile	Gly	Ser	Gly	Met	Leu	Pro	Phe	Met	Thr	Pro	Val	Phe	Leu
	275						280					285			
Gln	Ile	Gly	Leu	Gly	Phe	Ser	Pro	Phe	His	Ala	Gly	Leu	Met	Met	Ile
	290					295					300				
Pro	Met	Val	Leu	Gly	Ser	Met	Gly	Met	Lys	Arg	Ile	Val	Val	Gln	Val
305					310					315					320
Val	Asn	Arg	Phe	Gly	Tyr	Arg	Arg	Val	Leu	Val	Ala	Thr	Thr	Leu	Gly
			325					330						335	
Leu	Ser	Leu	Val	Thr	Leu	Leu	Phe	Met	Thr	Thr	Ala	Leu	Leu	Gly	Trp
			340					345					350		
Tyr	Tyr	Val	Leu	Pro	Phe	Val	Leu	Phe	Leu	Gln	Gly	Met	Val	Asn	Ser
	355						360					365			
Thr	Arg	Phe	Ser	Ser	Met	Asn	Thr	Leu	Thr	Leu	Lys	Asp	Leu	Pro	Asp
	370					375					380				
Asn	Leu	Ala	Ser	Ser	Gly	Asn	Ser	Leu	Leu	Ser	Met	Ile	Met	Gln	Leu
385					390					395					400
Ser	Met	Ser	Ile	Gly	Val	Thr	Ile	Ala	Gly	Leu	Leu	Leu	Gly	Leu	Phe
			405						410					415	
Gly	Ser	Gln	His	Val	Ser	Val	Asp	Ser	Gly	Thr	Thr	Gln	Thr	Val	Phe
			420				425					430			
Met	Tyr	Thr	Trp	Leu	Ser	Met	Ala	Leu	Ile	Ile	Ala	Leu	Pro	Ala	Phe
	435						440					445			
Ile	Phe	Ala	Arg	Val	Pro	Asn	Asp	Thr	His	Gln	Asn	Val	Ala	Ile	Ser
	450					455					460				
Arg	Arg	Lys	Arg	Ser	Ala	Gln									
465					470										

<210> 285
 <211> 344
 <212> PRT
 <213> E. Coli

<400> 285															
Met	Glu	Ile	Arg	Ile	Met	Leu	Phe	Ile	Leu	Met	Met	Met	Val	Met	Pro
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Val	Ser	Tyr	Ala	Ala	Cys	Tyr	Ser	Glu	Leu	Ser	Val	Gln	His	Asn	Leu
			20					25					30		
Val	Val	Gln	Gly	Asp	Phe	Ala	Leu	Thr	Gln	Thr	Gln	Met	Ala	Thr	Tyr
		35					40					45			
Glu	His	Asn	Phe	Asn	Asp	Ser	Ser	Cys	Val	Ser	Thr	Asn	Thr	Ile	Thr
	50					55					60				
Pro	Met	Ser	Pro	Ser	Asp	Ile	Ile	Val	Gly	Leu	Tyr	Asn	Asp	Thr	Ile
65					70					75					80
Lys	Leu	Asn	Leu	His	Phe	Glu	Trp	Thr	Asn	Lys	Asn	Asn	Ile	Thr	Leu

				85				90					95			
Ser	Asn	Asn	Gln	Thr	Ser	Phe	Thr	Ser	Gly	Tyr	Ser	Val	Thr	Val	Thr	
			100					105					110			
Pro	Ala	Ala	Ser	Asn	Ala	Lys	Val	Asn	Val	Ser	Ala	Gly	Gly	Gly	Gly	
		115					120					125				
Ser	Val	Met	Ile	Asn	Gly	Val	Ala	Thr	Leu	Ser	Ser	Ala	Ser	Ser	Ser	
	130				135					140						
Thr	Arg	Gly	Ser	Ala	Ala	Val	Gln	Phe	Leu	Leu	Cys	Leu	Leu	Gly	Gly	
145					150					155					160	
Lys	Ser	Trp	Asp	Ala	Cys	Val	Asn	Ser	Tyr	Arg	Asn	Ala	Leu	Ala	Gln	
			165						170					175		
Asn	Ala	Gly	Val	Tyr	Ser	Phe	Asn	Leu	Thr	Leu	Ser	Tyr	Asn	Pro	Ile	
			180					185					190			
Thr	Thr	Thr	Cys	Lys	Pro	Asp	Asp	Leu	Leu	Ile	Thr	Leu	Asp	Ser	Ile	
		195					200					205				
Pro	Val	Ser	Gln	Leu	Pro	Ala	Thr	Gly	Asn	Lys	Ala	Thr	Ile	Asn	Ser	
	210					215					220					
Lys	Gln	Gly	Asp	Ile	Ile	Leu	Arg	Cys	Lys	Asn	Leu	Leu	Gly	Gln	Gln	
225					230					235					240	
Asn	Gln	Thr	Ser	Arg	Lys	Met	Gln	Val	Tyr	Leu	Ser	Ser	Ser	Asp	Leu	
				245					250					255		
Leu	Thr	Asn	Ser	Asn	Thr	Ile	Leu	Lys	Gly	Ala	Glu	Asp	Asn	Gly	Val	
			260					265					270			
Gly	Phe	Ile	Leu	Glu	Ser	Asn	Gly	Ser	Pro	Val	Thr	Leu	Leu	Asn	Ile	
		275					280					285				
Thr	Asn	Ser	Ser	Lys	Gly	Tyr	Thr	Asn	Leu	Lys	Glu	Val	Ala	Ala	Lys	
	290					295					300					
Ser	Lys	Leu	Thr	Asp	Thr	Thr	Val	Ser	Ile	Pro	Ile	Thr	Ala	Ser	Tyr	
305					310					315					320	
Tyr	Val	Tyr	Asp	Thr	Asn	Lys	Val	Lys	Ser	Gly	Ala	Leu	Glu	Ala	Thr	
			325						330					335		
Ala	Leu	Ile	Asn	Val	Lys	Tyr	Asp									
			340													

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<211> 826

<212> PRT

<213> E. Coli

<400> 286

Met	Leu	Arg	Met	Thr	Pro	Leu	Ala	Ser	Ala	Ile	Val	Ala	Leu	Leu	Leu	
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Gly	Ile	Glu	Ala	Tyr	Ala	Ala	Glu	Glu	Thr	Phe	Asp	Thr	His	Phe	Met	
			20					25					30			
Ile	Gly	Gly	Met	Lys	Asp	Gln	Gln	Val	Ala	Asn	Ile	Arg	Leu	Asp	Asp	
		35				40						45				
Asn	Gln	Pro	Leu	Pro	Gly	Gln	Tyr	Asp	Ile	Asp	Ile	Tyr	Val	Asn	Lys	
	50				55					60						
Gln	Trp	Arg	Gly	Lys	Tyr	Glu	Ile	Ile	Val	Lys	Asp	Asn	Pro	Gln	Glu	
65					70					75					80	
Thr	Cys	Leu	Ser	Arg	Glu	Val	Ile	Lys	Arg	Leu	Gly	Ile	Asn	Ser	Asp	
				85					90				95			
Asn	Phe	Ala	Ser	Gly	Lys	Gln	Cys	Leu	Thr	Phe	Glu	Gln	Leu	Val	Gln	
		100						105					110			
Gly	Gly	Ser	Tyr	Thr	Trp	Asp	Ile	Gly	Val	Phe	Arg	Leu	Asp	Phe	Ser	
		115					120						125			

Val	Pro	Gln	Ala	Trp	Val	Glu	Glu	Leu	Glu	Ser	Gly	Tyr	Val	Pro	Pro
130						135					140				
Glu	Asn	Trp	Glu	Arg	Gly	Ile	Asn	Ala	Phe	Tyr	Thr	Ser	Tyr	Tyr	Leu
145					150					155					160
Ser	Gln	Tyr	Tyr	Ser	Asp	Tyr	Lys	Ala	Ser	Gly	Asn	Asn	Lys	Ser	Thr
				165					170						175
Tyr	Val	Arg	Phe	Asn	Ser	Gly	Leu	Asn	Leu	Leu	Gly	Trp	Gln	Leu	His
			180					185					190		
Ser	Asp	Ala	Ser	Phe	Ser	Lys	Thr	Asn	Asn	Asn	Pro	Gly	Val	Trp	Lys
	195						200					205			
Ser	Asn	Thr	Leu	Tyr	Leu	Glu	Arg	Gly	Phe	Ala	Gln	Leu	Leu	Gly	Thr
210						215					220				
Leu	Arg	Val	Gly	Asp	Met	Tyr	Thr	Ser	Ser	Asp	Ile	Phe	Asp	Ser	Val
225					230					235					240
Arg	Phe	Arg	Gly	Val	Arg	Leu	Phe	Arg	Asp	Met	Gln	Met	Leu	Pro	Asn
				245					250						255
Ser	Lys	Gln	Asn	Phe	Thr	Pro	Arg	Val	Gln	Gly	Ile	Ala	Gln	Ser	Asn
			260					265					270		
Ala	Leu	Val	Thr	Ile	Glu	Gln	Asn	Gly	Phe	Val	Val	Tyr	Gln	Lys	Glu
		275					280					285			
Val	Pro	Pro	Gly	Pro	Phe	Ala	Ile	Thr	Asp	Leu	Gln	Leu	Ala	Gly	Gly
290						295					300				
Gly	Ala	Asp	Leu	Asp	Val	Ser	Val	Lys	Glu	Ala	Asp	Gly	Ser	Val	Thr
305					310					315					320
Thr	Tyr	Leu	Val	Pro	Tyr	Ala	Ala	Val	Pro	Asn	Met	Leu	Gln	Pro	Gly
				325					330					335	
Val	Ser	Lys	Tyr	Asp	Leu	Ala	Ala	Gly	Arg	Ser	His	Ile	Glu	Gly	Ala
			340					345					350		
Ser	Lys	Gln	Ser	Asp	Phe	Val	Gln	Ala	Gly	Tyr	Gln	Tyr	Gly	Phe	Asn
	355						360					365			
Asn	Leu	Leu	Thr	Leu	Tyr	Gly	Gly	Ser	Met	Val	Ala	Asn	Asn	Tyr	Tyr
370						375					380				
Ala	Phe	Thr	Leu	Gly	Ala	Gly	Trp	Asn	Thr	Arg	Ile	Gly	Ala	Ile	Ser
385					390					395					400
Val	Asp	Ala	Thr	Lys	Ser	His	Ser	Lys	Gln	Asp	Asn	Gly	Asp	Val	Phe
				405					410					415	
Asp	Gly	Gln	Ser	Tyr	Gln	Ile	Ala	Tyr	Asn	Lys	Phe	Val	Ser	Gln	Thr
			420					425					430		
Ser	Thr	Arg	Phe	Gly	Leu	Ala	Ala	Trp	Arg	Tyr	Ser	Ser	Arg	Asp	Tyr
	435						440					445			
Arg	Thr	Phe	Asn	Asp	His	Val	Trp	Ala	Asn	Asn	Lys	Asp	Asn	Tyr	Arg
450						455					460				
Arg	Asp	Glu	Asn	Asp	Val	Tyr	Asp	Ile	Ala	Asp	Tyr	Tyr	Gln	Asn	Asp
465					470					475					480
Phe	Gly	Arg	Lys	Asn	Ser	Phe	Ser	Ala	Asn	Met	Ser	Gln	Ser	Leu	Pro
				485					490					495	
Glu	Gly	Trp	Gly	Ser	Val	Ser	Leu	Ser	Thr	Leu	Trp	Arg	Asp	Tyr	Trp
			500					505					510		
Gly	Arg	Ser	Gly	Ser	Ser	Lys	Asp	Tyr	Gln	Leu	Ser	Tyr	Ser	Asn	Asn
	515						520					525			
Leu	Arg	Arg	Ile	Ser	Tyr	Thr	Leu	Ala	Ala	Ser	Gln	Ala	Tyr	Asp	Glu
530						535					540				
Asn	His	His	Glu	Glu	Lys	Arg	Phe	Asn	Ile	Phe	Ile	Ser	Ile	Pro	Phe
545					550					555					560
Asp	Trp	Gly	Asp	Asp	Val	Ser	Thr	Pro	Arg	Arg	Gln	Ile	Tyr	Met	Ser
				565					570					575	
Asn	Ser	Thr	Thr	Phe	Asp	Asp	Gln	Gly	Phe	Ala	Ser	Asn	Asn	Thr	Gly

			580					585				590			
Leu	Ser	Gly	Thr	Val	Gly	Ser	Arg	Asp	Gln	Phe	Asn	Tyr	Gly	Val	Asn
		595					600					605			
Leu	Ser	His	Gln	His	Gln	Gly	Asn	Glu	Thr	Thr	Ala	Gly	Ala	Asn	Leu
	610					615					620				
Thr	Trp	Asn	Ala	Pro	Val	Ala	Thr	Val	Asn	Gly	Ser	Tyr	Ser	Gln	Ser
625					630					635					640
Ser	Thr	Tyr	Arg	Gln	Ala	Gly	Ala	Ser	Val	Ser	Gly	Gly	Ile	Val	Ala
			645						650					655	
Trp	Ser	Gly	Gly	Val	Asn	Leu	Ala	Asn	Arg	Leu	Ser	Glu	Thr	Phe	Ala
		660						665					670		
Val	Met	Asn	Ala	Pro	Gly	Ile	Lys	Asp	Ala	Tyr	Val	Asn	Gly	Gln	Lys
		675					680						685		
Tyr	Arg	Thr	Thr	Asn	Arg	Asn	Gly	Val	Val	Ile	Tyr	Asp	Gly	Met	Thr
	690					695						700			
Pro	Tyr	Arg	Glu	Asn	His	Leu	Met	Leu	Asp	Val	Ser	Gln	Ser	Asp	Ser
705					710						715				720
Glu	Ala	Glu	Leu	Arg	Gly	Asn	Arg	Lys	Ile	Ala	Ala	Pro	Tyr	Arg	Gly
				725						730				735	
Ala	Val	Val	Leu	Val	Asn	Phe	Asp	Thr	Asp	Gln	Arg	Lys	Pro	Trp	Phe
			740					745						750	
Ile	Lys	Ala	Leu	Arg	Ala	Asp	Gly	Gln	Ser	Leu	Thr	Phe	Gly	Tyr	Glu
		755					760						765		
Val	Asn	Asp	Ile	His	Gly	His	Asn	Ile	Gly	Val	Val	Gly	Gln	Gly	Ser
	770					775							780		
Gln	Leu	Phe	Ile	Arg	Thr	Asn	Glu	Val	Pro	Pro	Ser	Val	Asn	Val	Ala
785					790					795					800
Ile	Asp	Lys	Gln	Gln	Gly	Leu	Ser	Cys	Thr	Ile	Thr	Phe	Gly	Lys	Glu
			805						810					815	
Ile	Asp	Glu	Ser	Arg	Asn	Tyr	Ile	Cys	Gln						
			820					825							

<210> 287

<211> 239

<212> PRT

<213> E. Coli

<400> 287

Met	Ala	Ala	Ile	Pro	Trp	Arg	Pro	Phe	Asn	Leu	Arg	Gly	Ile	Lys	Met
1				5					10					15	
Lys	Gly	Leu	Leu	Ser	Leu	Leu	Ile	Phe	Ser	Met	Val	Leu	Pro	Ala	His
			20					25					30		
Ala	Gly	Ile	Val	Ile	Tyr	Gly	Thr	Arg	Ile	Ile	Tyr	Pro	Ala	Glu	Asn
		35				40						45			
Lys	Glu	Val	Met	Val	Gln	Leu	Met	Asn	Gln	Gly	Asn	Arg	Ser	Ser	Leu
	50					55					60				
Leu	Gln	Ala	Trp	Ile	Asp	Asp	Gly	Asp	Thr	Ser	Leu	Pro	Pro	Glu	Lys
65					70					75					80
Ile	Gln	Val	Pro	Phe	Met	Leu	Thr	Pro	Pro	Val	Ala	Lys	Ile	Gly	Ala
				85					90					95	
Asn	Ser	Gly	Gln	Gln	Val	Lys	Ile	Lys	Ile	Met	Pro	Asn	Lys	Leu	Pro
			100					105					110		
Thr	Asn	Lys	Glu	Ser	Ile	Phe	Tyr	Leu	Asn	Val	Leu	Asp	Ile	Pro	Pro
		115					120					125			
Asn	Ser	Pro	Glu	Gln	Glu	Gly	Lys	Asn	Ala	Leu	Lys	Phe	Ala	Met	Gln
		130				135						140			

Asn	Arg	Ile	Lys	Leu	Phe	Tyr	Arg	Pro	Ala	Gly	Ile	Ala	Pro	Val	Asn
145					150					155					160
Lys	Ala	Thr	Phe	Lys	Lys	Leu	Leu	Val	Asn	Arg	Ser	Gly	Asn	Gly	Leu
				165					170						175
Val	Ile	Lys	Asn	Asp	Ser	Ala	Asn	Trp	Val	Thr	Ile	Ser	Asp	Val	Lys
			180					185					190		
Ala	Asn	Asn	Val	Lys	Val	Asn	Tyr	Glu	Thr	Ile	Met	Ile	Ala	Pro	Leu
	195						200					205			
Glu	Ser	Gln	Ser	Val	Asn	Val	Lys	Ser	Asn	Asn	Ala	Asn	Asn	Trp	His
	210					215					220				
Leu	Thr	Ile	Ile	Asp	Asp	His	Gly	Asn	Tyr	Ile	Ser	Asp	Lys	Ile	
225					230					235					

<210> 288
 <211> 180
 <212> PRT
 <213> E. Coli

<400> 288

Met	Lys	Arg	Ser	Ile	Ile	Ala	Ala	Ala	Val	Phe	Ser	Ser	Phe	Phe	Met
1				5					10					15	
Ser	Ala	Gly	Val	Phe	Ala	Ala	Asp	Val	Asp	Thr	Gly	Thr	Leu	Thr	Ile
			20					25					30		
Lys	Gly	Asn	Ile	Ala	Glu	Ser	Pro	Cys	Lys	Phe	Glu	Ala	Gly	Gly	Asp
		35					40					45			
Ser	Val	Ser	Ile	Asn	Met	Pro	Thr	Val	Pro	Thr	Ser	Val	Phe	Glu	Gly
	50				55						60				
Lys	Ala	Lys	Tyr	Ser	Thr	Tyr	Asp	Asp	Ala	Val	Gly	Val	Thr	Ser	Ser
65					70					75					80
Met	Leu	Lys	Ile	Ser	Cys	Pro	Lys	Glu	Val	Ala	Gly	Val	Lys	Leu	Ser
			85					90						95	
Leu	Ile	Thr	Asn	Asp	Lys	Ile	Thr	Gly	Asn	Asp	Lys	Ala	Ile	Ala	Ser
			100					105					110		
Ser	Asn	Asp	Thr	Val	Gly	Tyr	Tyr	Leu	Tyr	Leu	Gly	Asp	Asn	Ser	Asp
		115					120					125			
Val	Leu	Asp	Val	Ser	Ala	Pro	Phe	Asn	Ile	Glu	Ser	Tyr	Lys	Thr	Ala
	130					135					140				
Glu	Gly	Gln	Tyr	Ala	Ile	Pro	Phe	Lys	Ala	Lys	Tyr	Leu	Lys	Leu	Thr
145					150					155					160
Asp	Asn	Ser	Val	Gln	Ser	Gly	Asp	Val	Leu	Ser	Ser	Leu	Val	Met	Arg
				165					170					175	
Val	Ala	Gln	Asp												
			180												

<210> 289
 <211> 112
 <212> PRT
 <213> E. Coli

<400> 289

Met	Ser	Ser	Glu	Arg	Asp	Leu	Val	Asn	Phe	Leu	Gly	Asp	Phe	Ser	Met
1				5					10					15	
Asp	Val	Ala	Lys	Ala	Val	Ile	Ala	Gly	Gly	Val	Ala	Thr	Ala	Ile	Gly
			20					25					30		

Ser	Leu	Ala	Ser	Phe	Ala	Cys	Val	Ser	Phe	Gly	Phe	Pro	Val	Ile	Leu
	35						40					45			
Val	Gly	Gly	Ala	Ile	Leu	Leu	Thr	Gly	Ile	Val	Cys	Thr	Val	Val	Leu
	50					55					60				
Asn	Glu	Ile	Asp	Ala	Gln	Cys	His	Leu	Ser	Glu	Lys	Leu	Lys	Tyr	Ala
65					70					75					80
Ile	Arg	Asp	Gly	Leu	Lys	Arg	Gln	Gln	Glu	Leu	Asp	Lys	Trp	Lys	Arg
			85						90					95	
Glu	Asn	Met	Thr	Pro	Phe	Met	Tyr	Val	Leu	Asn	Thr	Pro	Pro	Val	Ile
			100					105						110	

<210> 290
 <211> 193
 <212> PRT
 <213> E. Coli

<400> 290

Met	Thr	Asp	Tyr	Leu	Leu	Leu	Phe	Val	Gly	Thr	Val	Leu	Val	Asn	Asn
1				5					10					15	
Phe	Val	Leu	Val	Lys	Phe	Leu	Gly	Leu	Cys	Pro	Phe	Met	Gly	Val	Ser
			20					25					30		
Lys	Lys	Leu	Glu	Thr	Ala	Met	Gly	Met	Gly	Leu	Ala	Thr	Thr	Phe	Val
			35				40						45		
Met	Thr	Leu	Ala	Ser	Ile	Cys	Ala	Trp	Leu	Ile	Asp	Thr	Trp	Ile	Leu
			50			55					60				
Ile	Pro	Leu	Asn	Leu	Ile	Tyr	Leu	Arg	Thr	Leu	Ala	Phe	Ile	Leu	Val
65					70					75					80
Ile	Ala	Val	Val	Val	Gln	Phe	Thr	Glu	Met	Val	Val	Arg	Lys	Thr	Ser
				85					90					95	
Pro	Val	Leu	Tyr	Arg	Leu	Leu	Gly	Ile	Phe	Leu	Pro	Leu	Ile	Thr	Thr
			100					105						110	
Asn	Cys	Ala	Val	Leu	Gly	Val	Ala	Leu	Leu	Asn	Ile	Asn	Leu	Gly	His
		115					120					125			
Asn	Phe	Leu	Gln	Ser	Ala	Leu	Tyr	Gly	Phe	Ser	Ala	Ala	Val	Gly	Phe
		130				135					140				
Ser	Leu	Val	Met	Val	Leu	Phe	Ala	Ala	Ile	Arg	Glu	Arg	Leu	Ala	Val
145					150					155					160
Ala	Asp	Val	Pro	Ala	Pro	Phe	Arg	Gly	Asn	Ala	Ile	Ala	Leu	Ile	Thr
				165					170					175	
Ala	Gly	Leu	Met	Ser	Leu	Ala	Phe	Met	Gly	Phe	Ser	Gly	Leu	Val	Lys
			180					185						190	

Leu

<210> 291
 <211> 192
 <212> PRT
 <213> E. Coli

<400> 291

Met	Asn	Ala	Ile	Trp	Ile	Ala	Val	Ala	Ala	Val	Ser	Leu	Leu	Gly	Leu
1				5				10						15	
Ala	Phe	Gly	Ala	Ile	Leu	Gly	Tyr	Ala	Ser	Arg	Arg	Phe	Ala	Val	Glu
			20					25						30	

Asp	Asp	Pro	Val	Val	Glu	Lys	Ile	Asp	Glu	Ile	Leu	Pro	Gln	Ser	Gln
	35						40					45			
Cys	Gly	Gln	Cys	Gly	Tyr	Pro	Gly	Cys	Arg	Pro	Tyr	Ala	Glu	Ala	Ile
	50					55					60				
Ser	Cys	Asn	Gly	Glu	Lys	Ile	Asn	Arg	Cys	Ala	Pro	Gly	Gly	Glu	Ala
65					70					75					80
Val	Met	Leu	Lys	Ile	Ala	Glu	Leu	Leu	Asn	Val	Glu	Pro	Gln	Pro	Leu
			85						90					95	
Asp	Gly	Glu	Ala	Gln	Glu	Ile	Thr	Pro	Ala	Arg	Met	Val	Ala	Val	Ile
			100					105					110		
Asp	Glu	Asn	Asn	Cys	Ile	Gly	Cys	Thr	Lys	Cys	Ile	Gln	Ala	Cys	Pro
		115					120					125			
Val	Asp	Ala	Ile	Val	Gly	Ala	Thr	Arg	Ala	Met	His	Thr	Val	Met	Ser
	130					135					140				
Asp	Leu	Cys	Thr	Gly	Cys	Asn	Leu	Cys	Val	Asp	Pro	Cys	Pro	Thr	His
145					150					155					160
Cys	Ile	Ser	Leu	Gln	Pro	Val	Ala	Glu	Thr	Pro	Asp	Ser	Trp	Lys	Trp
				165					170					175	
Asp	Leu	Asn	Thr	Ile	Pro	Val	Arg	Ile	Ile	Pro	Val	Glu	His	His	Ala
			180					185					190		

<210> 292
 <211> 740
 <212> PRT
 <213> E. Coli

<400> 292

Met	Leu	Lys	Leu	Phe	Ser	Ala	Phe	Arg	Lys	Asn	Lys	Ile	Trp	Asp	Phe
1				5					10					15	
Asn	Gly	Gly	Ile	His	Pro	Pro	Glu	Met	Lys	Thr	Gln	Ser	Asn	Gly	Thr
			20					25					30		
Pro	Leu	Arg	Gln	Val	Pro	Leu	Ala	Gln	Arg	Phe	Val	Ile	Pro	Leu	Lys
		35					40					45			
Gln	His	Ile	Gly	Ala	Glu	Gly	Glu	Leu	Cys	Val	Ser	Val	Gly	Asp	Lys
	50					55					60				
Val	Leu	Arg	Gly	Gln	Pro	Leu	Thr	Arg	Gly	Arg	Gly	Lys	Met	Leu	Pro
65					70					75					80
Val	His	Ala	Pro	Thr	Ser	Gly	Thr	Val	Thr	Ala	Ile	Ala	Pro	His	Ser
				85					90					95	
Thr	Ala	His	Pro	Ser	Ala	Leu	Ala	Glu	Leu	Ser	Val	Ile	Ile	Asp	Ala
			100					105					110		
Asp	Gly	Glu	Asp	Cys	Trp	Ile	Pro	Arg	Asp	Gly	Trp	Ala	Asp	Tyr	Arg
		115					120					125			
Thr	Arg	Ser	Arg	Glu	Glu	Leu	Ile	Glu	Arg	Ile	His	Gln	Phe	Gly	Val
	130					135					140				
Ala	Gly	Leu	Gly	Gly	Ala	Gly	Phe	Pro	Thr	Gly	Val	Lys	Leu	Gln	Gly
145					150					155					160
Gly	Gly	Asp	Lys	Ile	Glu	Thr	Leu	Ile	Ile	Asn	Ala	Ala	Glu	Cys	Glu
				165					170					175	
Pro	Tyr	Ile	Thr	Ala	Asp	Asp	Arg	Leu	Met	Gln	Asp	Cys	Ala	Ala	Gln
			180					185					190		
Val	Val	Glu	Gly	Ile	Arg	Ile	Leu	Ala	His	Ile	Leu	Gln	Pro	Arg	Glu
		195					200					205			
Ile	Leu	Ile	Gly	Ile	Glu	Asp	Asn	Lys	Pro	Gln	Ala	Ile	Ser	Met	Leu
	210					215					220				
Arg	Ala	Val	Leu	Ala	Asp	Ser	Asn	Asp	Ile	Ser	Leu	Arg	Val	Ile	Pro

225					230					235					240
Thr	Lys	Tyr	Pro	Ser	Gly	Gly	Ala	Lys	Gln	Leu	Thr	Tyr	Ile	Leu	Thr
				245					250					255	
Gly	Lys	Gln	Val	Pro	His	Gly	Gly	Arg	Ser	Ser	Asp	Ile	Gly	Val	Leu
			260					265					270		
Met	Gln	Asn	Val	Gly	Thr	Ala	Tyr	Ala	Val	Lys	Arg	Ala	Val	Ile	Asp
		275					280					285			
Gly	Glu	Pro	Ile	Thr	Glu	Arg	Val	Val	Thr	Leu	Thr	Gly	Glu	Ala	Ile
	290					295				300					
Ala	Arg	Pro	Gly	Asn	Val	Trp	Ala	Arg	Leu	Gly	Thr	Pro	Val	Arg	His
305				310						315					320
Leu	Leu	Asn	Asp	Ala	Gly	Phe	Cys	Pro	Ser	Ala	Asp	Gln	Met	Val	Ile
			325						330					335	
Met	Gly	Gly	Pro	Leu	Met	Gly	Phe	Thr	Leu	Pro	Trp	Leu	Asp	Val	Pro
			340					345					350		
Val	Val	Lys	Ile	Thr	Asn	Cys	Leu	Leu	Ala	Pro	Ser	Ala	Asn	Glu	Leu
		355					360					365			
Gly	Glu	Pro	Gln	Glu	Glu	Gln	Ser	Cys	Ile	Arg	Cys	Ser	Ala	Cys	Ala
	370					375					380				
Asp	Ala	Cys	Pro	Ala	Asp	Leu	Leu	Pro	Gln	Gln	Leu	Tyr	Trp	Phe	Ser
385					390					395					400
Lys	Gly	Gln	Gln	His	Asp	Lys	Ala	Thr	Thr	His	Asn	Ile	Ala	Asp	Cys
				405					410					415	
Ile	Glu	Cys	Gly	Ala	Cys	Ala	Trp	Val	Cys	Pro	Ser	Asn	Ile	Pro	Leu
			420					425					430		
Val	Gln	Tyr	Phe	Arg	Gln	Glu	Lys	Ala	Glu	Ile	Ala	Ala	Ile	Arg	Gln
		435					440					445			
Glu	Glu	Lys	Arg	Ala	Ala	Glu	Ala	Lys	Ala	Arg	Phe	Glu	Ala	Arg	Gln
	450					455					460				
Ala	Arg	Leu	Glu	Arg	Glu	Lys	Ala	Ala	Arg	Leu	Glu	Arg	His	Lys	Ser
465					470					475					480
Ala	Ala	Val	Gln	Pro	Ala	Ala	Lys	Asp	Lys	Asp	Ala	Ile	Ala	Ala	Ala
			485						490					495	
Leu	Ala	Arg	Val	Lys	Glu	Lys	Gln	Ala	Gln	Ala	Thr	Gln	Pro	Ile	Val
			500					505					510		
Ile	Lys	Ala	Gly	Glu	Arg	Pro	Asp	Asn	Ser	Ala	Ile	Ile	Ala	Ala	Arg
	515						520					525			
Glu	Ala	Arg	Lys	Ala	Gln	Ala	Arg	Ala	Lys	Gln	Ala	Glu	Leu	Gln	Gln
	530					535					540				
Thr	Asn	Asp	Ala	Ala	Thr	Val	Ala	Asp	Pro	Arg	Lys	Thr	Ala	Val	Glu
545					550					555					560
Ala	Ala	Ile	Ala	Arg	Ala	Lys	Ala	Arg	Lys	Leu	Glu	Gln	Gln	Gln	Ala
			565						570					575	
Asn	Ala	Glu	Pro	Glu	Gln	Gln	Val	Asp	Pro	Arg	Lys	Ala	Ala	Val	Glu
			580					585					590		
Ala	Ala	Ile	Ala	Arg	Ala	Lys	Ala	Arg	Lys	Leu	Glu	Gln	Gln	Gln	Ala
		595					600					605			
Asn	Ala	Glu	Pro	Glu	Glu	Gln	Val	Asp	Pro	Arg	Lys	Ala	Ala	Val	Glu
	610					615					620				
Ala	Ala	Ile	Ala	Arg	Ala	Lys	Ala	Arg	Lys	Leu	Glu	Gln	Gln	Gln	Ala
625					630					635					640
Asn	Ala	Glu	Pro	Glu	Gln	Gln	Val	Asp	Pro	Arg	Lys	Ala	Ala	Val	Glu
			645						650					655	
Ala	Ala	Ile	Ala	Arg	Ala	Lys	Ala	Arg	Lys	Arg	Glu	Gln	Gln	Pro	Ala
		660						665					670		
Asn	Ala	Glu	Pro	Glu	Glu	Gln	Val	Asp	Pro	Arg	Lys	Ala	Ala	Val	Glu
	675						680					685			

Ala	Ala	Ile	Ala	Arg	Ala	Lys	Ala	Arg	Lys	Leu	Glu	Gln	Gln	Gln	Ala
690						695					700				
Asn	Ala	Val	Pro	Glu	Glu	Gln	Val	Asp	Pro	Arg	Lys	Ala	Ala	Val	Ala
705					710					715					720
Ala	Ala	Ile	Ala	Arg	Ala	Gln	Ala	Lys	Lys	Ala	Ala	Gln	Gln	Lys	Val
				725					730					735	
Val	Asn	Glu	Asp												
			740												

<210> 293
 <211> 352
 <212> PRT
 <213> E. Coli

<400> 293

Met	Val	Phe	Arg	Ile	Ala	Ser	Ser	Pro	Tyr	Thr	His	Asn	Gln	Arg	Gln
1				5					10					15	
Thr	Ser	Arg	Ile	Met	Leu	Leu	Val	Leu	Leu	Ala	Ala	Val	Pro	Gly	Ile
			20					25					30		
Ala	Ala	Gln	Leu	Trp	Phe	Phe	Gly	Trp	Gly	Thr	Leu	Val	Gln	Ile	Leu
		35					40					45			
Leu	Ala	Ser	Val	Ser	Ala	Leu	Leu	Ala	Glu	Ala	Leu	Val	Leu	Lys	Leu
	50					55					60				
Arg	Lys	Gln	Ser	Val	Ala	Ala	Thr	Leu	Lys	Asp	Asn	Ser	Ala	Leu	Leu
65					70					75					80
Thr	Gly	Leu	Leu	Leu	Ala	Val	Ser	Ile	Pro	Pro	Leu	Ala	Pro	Trp	Trp
			85						90					95	
Met	Val	Val	Leu	Gly	Thr	Val	Phe	Ala	Val	Ile	Ile	Ala	Lys	Gln	Leu
			100					105					110		
Tyr	Gly	Gly	Leu	Gly	Gln	Asn	Pro	Phe	Asn	Pro	Ala	Met	Ile	Gly	Tyr
		115				120						125			
Val	Val	Leu	Leu	Ile	Ser	Phe	Pro	Val	Gln	Met	Thr	Ser	Trp	Leu	Pro
	130					135					140				
Pro	His	Glu	Ile	Ala	Val	Asn	Ile	Pro	Gly	Phe	Ile	Asp	Ala	Ile	Gln
145					150					155					160
Val	Ile	Phe	Ser	Gly	His	Thr	Ala	Ser	Gly	Gly	Asp	Met	Asn	Thr	Leu
				165					170					175	
Arg	Leu	Gly	Ile	Asp	Gly	Ile	Ser	Gln	Ala	Thr	Pro	Leu	Asp	Thr	Phe
			180					185					190		
Lys	Thr	Ser	Val	Arg	Ala	Gly	His	Ser	Val	Glu	Gln	Ile	Met	Gln	Tyr
		195				200						205			
Pro	Ile	Tyr	Ser	Gly	Ile	Leu	Ala	Gly	Ala	Gly	Trp	Gln	Trp	Val	Asn
	210					215					220				
Leu	Ala	Trp	Leu	Ala	Gly	Gly	Val	Trp	Leu	Leu	Trp	Gln	Lys	Ala	Ile
225					230					235					240
Arg	Trp	His	Ile	Pro	Leu	Ser	Phe	Leu	Val	Thr	Leu	Ala	Leu	Cys	Ala
				245					250					255	
Met	Leu	Gly	Trp	Leu	Phe	Ser	Pro	Glu	Thr	Leu	Ala	Ala	Pro	Gln	Ile
			260					265					270		
His	Leu	Leu	Ser	Gly	Ala	Thr	Met	Leu	Gly	Ala	Phe	Phe	Ile	Leu	Thr
		275					280					285			
Asp	Pro	Val	Thr	Ala	Ser	Thr	Thr	Asn	Arg	Gly	Arg	Leu	Ile	Phe	Gly
	290					295					300				
Ala	Leu	Ala	Gly	Leu	Leu	Val	Trp	Leu	Ile	Arg	Ser	Phe	Gly	Gly	Tyr
305					310					315					320

Pro	Asp	Gly	Val	Ala	Phe	Ala	Val	Leu	Leu	Ala	Asn	Ile	Thr	Val	Pro
				325					330					335	
Leu	Ile	Asp	Tyr	Tyr	Thr	Arg	Pro	Arg	Val	Tyr	Gly	His	Arg	Lys	Gly
			340					345						350	

<210> 294
 <211> 206
 <212> PRT
 <213> E. Coli

<400> 294

Met	Leu	Lys	Thr	Ile	Arg	Lys	His	Gly	Ile	Thr	Leu	Ala	Leu	Phe	Ala
1				5					10					15	
Ala	Gly	Ser	Thr	Gly	Leu	Thr	Ala	Ala	Ile	Asn	Gln	Met	Thr	Lys	Thr
			20					25					30		
Thr	Ile	Ala	Glu	Gln	Ala	Ser	Leu	Gln	Gln	Lys	Ala	Leu	Phe	Asp	Gln
		35					40					45			
Val	Leu	Pro	Ala	Glu	Arg	Tyr	Asn	Asn	Ala	Leu	Ala	Gln	Ser	Cys	Tyr
	50					55					60				
Leu	Val	Thr	Ala	Pro	Glu	Leu	Gly	Lys	Gly	Glu	His	Arg	Val	Tyr	Ile
65					70					75					80
Ala	Lys	Gln	Asp	Asp	Lys	Pro	Val	Ala	Ala	Val	Leu	Glu	Ala	Thr	Ala
			85						90					95	
Pro	Asp	Gly	Tyr	Ser	Gly	Ala	Ile	Gln	Leu	Leu	Val	Gly	Ala	Asp	Phe
			100					105					110		
Asn	Gly	Thr	Val	Leu	Gly	Thr	Arg	Val	Thr	Glu	His	His	Glu	Thr	Pro
		115					120					125			
Gly	Leu	Gly	Asp	Lys	Ile	Glu	Leu	Arg	Leu	Ser	Asp	Trp	Ile	Thr	His
	130					135					140				
Phe	Ala	Gly	Lys	Lys	Ile	Ser	Gly	Ala	Asp	Asp	Ala	His	Trp	Ala	Val
145					150					155					160
Lys	Lys	Asp	Gly	Gly	Asp	Phe	Asp	Gln	Phe	Thr	Gly	Ala	Thr	Ile	Thr
			165						170					175	
Pro	Arg	Ala	Val	Val	Asn	Ala	Val	Lys	Arg	Ala	Gly	Leu	Tyr	Ala	Gln
			180					185					190		
Thr	Leu	Pro	Ala	Gln	Leu	Ser	Gln	Leu	Pro	Ala	Cys	Gly	Glu		
		195					200					205			

<210> 295
 <211> 231
 <212> PRT
 <213> E. Coli

<400> 295

Met	Ser	Glu	Ile	Lys	Asp	Val	Ile	Val	Gln	Gly	Leu	Trp	Lys	Asn	Asn
1				5					10					15	
Ser	Ala	Leu	Val	Gln	Leu	Leu	Gly	Leu	Cys	Pro	Leu	Leu	Ala	Val	Thr
			20					25					30		
Ser	Thr	Ala	Thr	Asn	Ala	Leu	Gly	Leu	Gly	Leu	Ala	Thr	Thr	Leu	Val
		35					40					45			
Leu	Thr	Leu	Thr	Asn	Leu	Thr	Ile	Ser	Thr	Leu	Arg	His	Trp	Thr	Pro
	50					55					60				
Ala	Glu	Ile	Arg	Ile	Pro	Ile	Tyr	Val	Met	Ile	Ile	Ala	Ser	Val	Val
65					70					75					80
Ser	Ala	Val	Gln	Met	Leu	Ile	Asn	Ala	Tyr	Ala	Phe	Gly	Leu	Tyr	Gln

				85					90				95			
Ser	Leu	Gly	Ile	Phe	Ile	Pro	Leu	Ile	Val	Thr	Asn	Cys	Ile	Val	Val	
			100					105					110			
Gly	Arg	Ala	Glu	Ala	Phe	Ala	Ala	Lys	Lys	Gly	Pro	Ala	Leu	Ser	Ala	
		115					120					125				
Leu	Asp	Gly	Phe	Ser	Ile	Gly	Met	Gly	Ala	Thr	Cys	Ala	Met	Phe	Val	
	130					135					140					
Leu	Gly	Ser	Leu	Arg	Glu	Ile	Ile	Gly	Asn	Gly	Thr	Leu	Phe	Asp	Gly	
145					150				155						160	
Ala	Asp	Ala	Leu	Leu	Gly	Ser	Trp	Ala	Lys	Val	Leu	Arg	Val	Glu	Ile	
			165					170						175		
Phe	His	Thr	Asp	Ser	Pro	Phe	Leu	Leu	Ala	Met	Leu	Pro	Pro	Gly	Ala	
			180				185						190			
Phe	Ile	Gly	Leu	Gly	Leu	Met	Leu	Ala	Gly	Lys	Tyr	Leu	Ile	Asp	Glu	
		195					200					205				
Arg	Met	Lys	Lys	Arg	Arg	Ala	Glu	Ala	Ala	Ala	Glu	Arg	Ala	Leu	Pro	
	210					215					220					
Asn	Gly	Glu	Thr	Gly	Asn	Val										
225					230											

<210> 296
 <211> 211
 <212> PRT
 <213> E. Coli

Met	Asn	Lys	Ala	Lys	Arg	Leu	Glu	Ile	Leu	Thr	Arg	Leu	Arg	Glu	Asn	
1				5					10					15		
Asn	Pro	His	Pro	Thr	Thr	Glu	Leu	Asn	Phe	Ser	Ser	Pro	Phe	Glu	Leu	
			20					25					30			
Leu	Ile	Ala	Val	Leu	Leu	Ser	Ala	Gln	Ala	Thr	Asp	Val	Ser	Val	Asn	
		35					40					45				
Lys	Ala	Thr	Ala	Lys	Leu	Tyr	Pro	Val	Ala	Asn	Thr	Pro	Ala	Ala	Met	
	50					55					60					
Leu	Glu	Leu	Gly	Val	Glu	Gly	Val	Lys	Thr	Tyr	Ile	Lys	Thr	Ile	Gly	
65					70					75					80	
Leu	Tyr	Asn	Ser	Lys	Ala	Glu	Asn	Ile	Ile	Lys	Thr	Cys	Arg	Ile	Leu	
				85				90						95		
Leu	Glu	Gln	His	Asn	Gly	Glu	Val	Pro	Glu	Asp	Arg	Ala	Ala	Leu	Glu	
			100					105					110			
Ala	Leu	Pro	Gly	Val	Gly	Arg	Lys	Thr	Ala	Asn	Val	Val	Leu	Asn	Thr	
		115					120					125				
Ala	Phe	Gly	Trp	Pro	Thr	Ile	Ala	Val	Asp	Thr	His	Ile	Phe	Arg	Val	
	130					135					140					
Cys	Asn	Arg	Thr	Gln	Phe	Ala	Pro	Gly	Lys	Asn	Val	Glu	Gln	Val	Glu	
145					150				155						160	
Glu	Lys	Leu	Leu	Lys	Val	Val	Pro	Ala	Glu	Phe	Lys	Val	Asp	Cys	His	
			165					170						175		
His	Trp	Leu	Ile	Leu	His	Gly	Arg	Tyr	Thr	Cys	Ile	Ala	Arg	Lys	Pro	
		180					185						190			
Arg	Cys	Gly	Ser	Cys	Ile	Ile	Glu	Asp	Leu	Cys	Glu	Tyr	Lys	Glu	Lys	
		195					200					205				
Val	Asp	Ile														
	210															

<210> 297
 <211> 167
 <212> PRT
 <213> E. Coli

<400> 297

Met	Lys	Arg	Leu	His	Lys	Arg	Phe	Leu	Leu	Ala	Thr	Phe	Cys	Ala	Leu
1				5					10					15	
Phe	Thr	Ala	Thr	Leu	Gln	Ala	Ala	Asp	Val	Thr	Ile	Thr	Val	Asn	Gly
			20					25					30		
Arg	Val	Val	Ala	Lys	Pro	Cys	Thr	Ile	Gln	Thr	Lys	Glu	Ala	Asn	Val
		35					40					45			
Asn	Leu	Gly	Asp	Leu	Tyr	Thr	Arg	Asn	Leu	Gln	Gln	Pro	Gly	Ser	Ala
	50					55					60				
Ser	Gly	Trp	His	Asn	Ile	Thr	Leu	Ser	Leu	Thr	Asp	Cys	Pro	Val	Glu
65					70					75					80
Thr	Ser	Ala	Val	Thr	Ala	Ile	Val	Thr	Gly	Ser	Thr	Asp	Asn	Thr	Gly
				85					90					95	
Tyr	Tyr	Lys	Asn	Glu	Gly	Thr	Ala	Glu	Asn	Ile	Gln	Ile	Glu	Leu	Arg
			100					105					110		
Asp	Asp	Gln	Asp	Ala	Ala	Leu	Lys	Asn	Gly	Asp	Ser	Lys	Thr	Val	Ile
		115					120					125			
Val	Asp	Glu	Ile	Thr	Arg	Asn	Ala	Gln	Phe	Pro	Leu	Lys	Ala	Arg	Ala
	130					135					140				
Ile	Thr	Val	Asn	Gly	Asn	Ala	Ser	Gln	Gly	Thr	Ile	Glu	Ala	Leu	Ile
145					150					155					160
Asn	Val	Ile	Tyr	Thr	Trp	Gln									
				165											

<210> 298
 <211> 176
 <212> PRT
 <213> E. Coli

<400> 298

Met	Lys	Tyr	Asn	Asn	Ile	Ile	Phe	Leu	Gly	Leu	Cys	Leu	Gly	Leu	Thr
1				5					10					15	
Thr	Tyr	Ser	Ala	Leu	Ser	Ala	Asp	Ser	Val	Ile	Lys	Ile	Ser	Gly	Arg
			20					25					30		
Val	Leu	Asp	Tyr	Gly	Cys	Thr	Val	Ser	Ser	Asp	Ser	Leu	Asn	Phe	Thr
		35					40					45			
Val	Asp	Leu	Gln	Lys	Asn	Ser	Ala	Arg	Gln	Phe	Pro	Thr	Thr	Gly	Ser
	50				55						60				
Thr	Ser	Pro	Ala	Val	Pro	Phe	Gln	Ile	Thr	Leu	Ser	Glu	Cys	Ser	Lys
65					70					75					80
Gly	Thr	Thr	Gly	Val	Arg	Val	Ala	Phe	Asn	Gly	Ile	Glu	Asp	Ala	Glu
				85					90					95	
Asn	Asn	Thr	Leu	Lys	Leu	Asp	Glu	Gly	Ser	Asn	Thr	Ala	Ser	Gly	
			100				105					110			
Leu	Gly	Ile	Glu	Ile	Leu	Asp	Ala	Asn	Met	Arg	Pro	Val	Lys	Leu	Asn
		115					120					125			
Asp	Leu	His	Ala	Gly	Met	Gln	Trp	Ile	Pro	Leu	Val	Pro	Glu	Gln	Asn
	130					135					140				
Asn	Ile	Leu	Pro	Tyr	Ser	Ala	Arg	Leu	Lys	Ser	Thr	Gln	Lys	Ser	Val
145					150					155					160

Asn	Pro	Gly	Leu	Val	Arg	Ala	Ser	Ala	Thr	Phe	Thr	Leu	Glu	Phe	Gln
				165					170					175	

<210> 299
 <211> 382
 <212> PRT
 <213> E. Coli

<400> 299

Met	Ser	Gly	Tyr	Thr	Val	Lys	Pro	Pro	Thr	Gly	Asp	Thr	Asn	Glu	Gln
1				5					10					15	
Thr	Gln	Phe	Ile	Asp	Tyr	Phe	Asn	Leu	Phe	Tyr	Ser	Lys	Arg	Gly	Gln
			20					25					30		
Glu	Gln	Ile	Ser	Ile	Ser	Gln	Gln	Leu	Gly	Asn	Tyr	Gly	Thr	Thr	Phe
		35					40					45			
Phe	Ser	Ala	Ser	Arg	Gln	Ser	Tyr	Trp	Asn	Thr	Ser	Arg	Ser	Asp	Gln
	50					55					60				
Gln	Ile	Ser	Phe	Gly	Leu	Asn	Val	Pro	Phe	Gly	Asp	Ile	Thr	Thr	Ser
65					70					75					80
Leu	Asn	Tyr	Ser	Tyr	Ser	Asn	Asn	Ile	Trp	Gln	Asn	Asp	Arg	Asp	His
				85					90					95	
Leu	Leu	Ala	Phe	Thr	Leu	Asn	Val	Pro	Phe	Ser	His	Trp	Met	Arg	Thr
			100					105					110		
Asp	Ser	Gln	Ser	Ala	Phe	Arg	Asn	Ser	Asn	Ala	Ser	Tyr	Ser	Met	Ser
		115					120					125			
Asn	Asp	Leu	Lys	Gly	Gly	Met	Thr	Asn	Leu	Ser	Gly	Val	Tyr	Gly	Thr
	130					135					140				
Leu	Leu	Pro	Asp	Asn	Asn	Leu	Asn	Tyr	Ser	Val	Gln	Val	Gly	Asn	Thr
	145				150					155					160
His	Gly	Gly	Asn	Thr	Ser	Ser	Gly	Thr	Ser	Gly	Tyr	Ser	Ser	Leu	Asn
				165					170					175	
Tyr	Arg	Gly	Ala	Tyr	Gly	Asn	Thr	Asn	Val	Gly	Tyr	Ser	Arg	Ser	Gly
			180					185					190		
Asp	Ser	Ser	Gln	Ile	Tyr	Tyr	Gly	Met	Ser	Gly	Gly	Ile	Ile	Ala	His
		195					200					205			
Ala	Asp	Gly	Ile	Thr	Phe	Gly	Gln	Pro	Leu	Gly	Asp	Thr	Met	Val	Leu
	210					215					220				
Val	Lys	Ala	Pro	Gly	Ala	Asp	Asn	Val	Lys	Ile	Glu	Asn	Gln	Thr	Gly
	225				230					235					240
Ile	His	Thr	Asp	Trp	Arg	Gly	Tyr	Ala	Ile	Leu	Pro	Phe	Ala	Thr	Glu
				245					250					255	
Tyr	Arg	Glu	Asn	Arg	Val	Ala	Leu	Asn	Ala	Asn	Ser	Leu	Ala	Asp	Asn
			260					265					270		
Val	Glu	Leu	Asp	Glu	Thr	Val	Val	Thr	Val	Ile	Pro	Thr	His	Gly	Ala
	275						280					285			
Ile	Ala	Arg	Ala	Thr	Phe	Asn	Ala	Gln	Ile	Gly	Gly	Lys	Val	Leu	Met
	290					295					300				
Thr	Leu	Lys	Tyr	Gly	Asn	Lys	Ser	Val	Pro	Phe	Gly	Ala	Ile	Val	Thr
	305				310					315					320
His	Gly	Glu	Asn	Lys	Asn	Gly	Ser	Ile	Val	Ala	Glu	Asn	Gly	Gln	Val
				325					330					335	
Tyr	Leu	Thr	Gly	Leu	Pro	Gln	Ser	Gly	Gln	Leu	Gln	Val	Ser	Trp	Gly
			340					345					350		
Lys	Asp	Lys	Asn	Ser	Asn	Cys	Ile	Val	Glu	Tyr	Lys	Leu	Pro	Glu	Val
		355					360					365			

Ser Pro Gly Thr Leu Leu Asn Gln Gln Thr Ala Ile Cys Arg
 370 375 380

<210> 300
 <211> 138
 <212> PRT
 <213> E. Coli

<400> 300
 Met Ile Ala Ile Ala Asp Ile Leu Gln Ala Gly Glu Lys Leu Thr Ala
 1 5 10 15
 Val Ala Pro Phe Leu Ala Gly Ile Gln Asn Glu Glu Gln Tyr Thr Gln
 20 25 30
 Ala Leu Glu Leu Val Asp His Leu Leu Asn Asp Pro Glu Asn Pro
 35 40 45
 Leu Leu Asp Leu Val Cys Ala Lys Ile Thr Ala Trp Glu Glu Ser Ala
 50 55 60
 Pro Glu Phe Ala Glu Phe Asn Ala Met Ala Gln Ala Met Pro Gly Gly
 65 70 75 80
 Ile Ala Val Ile Arg Thr Leu Met Asp Gln Tyr Gly Leu Thr Leu Ser
 85 90 95
 Asp Leu Pro Glu Ile Gly Ser Lys Ser Met Val Ser Arg Val Leu Ser
 100 105 110
 Gly Lys Arg Lys Leu Thr Leu Glu His Ala Lys Lys Leu Ala Thr Arg
 115 120 125
 Phe Gly Ile Ser Pro Ala Leu Phe Ile Asp
 130 135

<210> 301
 <211> 104
 <212> PRT
 <213> E. Coli

<400> 301
 Met His Leu Ile Thr Gln Lys Ala Leu Lys Asp Ala Ala Glu Lys Tyr
 1 5 10 15
 Pro Gln His Lys Thr Glu Leu Val Ala Leu Gly Asn Thr Ile Ala Lys
 20 25 30
 Gly Tyr Phe Lys Lys Pro Glu Ser Leu Lys Ala Val Phe Pro Ser Leu
 35 40 45
 Asp Asn Phe Lys Tyr Leu Asp Lys His Tyr Val Phe Asn Val Gly Gly
 50 55 60
 Asn Glu Leu Arg Val Val Ala Met Val Phe Phe Glu Ser Gln Lys Cys
 65 70 75 80
 Tyr Ile Arg Glu Val Met Thr His Lys Glu Tyr Asp Phe Phe Thr Ala
 85 90 95
 Val His Arg Thr Lys Gly Lys Lys
 100

<210> 302
 <211> 2383
 <212> PRT
 <213> E. Coli

<400> 302

Met	Leu	Ser	Val	Phe	Thr	Phe	Phe	Arg	Cys	Ala	Arg	Lys	Gly	Ala	Phe
1				5					10					15	
Met	Leu	Ala	Arg	Ser	Gly	Lys	Val	Ser	Met	Ala	Thr	Lys	Lys	Arg	Ser
			20					25					30		
Gly	Glu	Glu	Ile	Asn	Asp	Arg	Gln	Ile	Leu	Cys	Gly	Met	Gly	Ile	Lys
			35				40					45			
Leu	Arg	Arg	Leu	Thr	Ala	Gly	Ile	Cys	Leu	Ile	Thr	Gln	Leu	Ala	Phe
			50			55					60				
Pro	Met	Ala	Ala	Ala	Ala	Gln	Gly	Val	Val	Asn	Ala	Ala	Thr	Gln	Gln
65					70					75					80
Pro	Val	Pro	Ala	Gln	Ile	Ala	Ile	Ala	Asn	Ala	Asn	Thr	Val	Pro	Tyr
				85					90					95	
Thr	Leu	Gly	Ala	Leu	Glu	Ser	Ala	Gln	Ser	Val	Ala	Glu	Arg	Phe	Gly
			100					105					110		
Ile	Ser	Val	Ala	Glu	Leu	Arg	Lys	Leu	Asn	Gln	Phe	Arg	Thr	Phe	Ala
			115				120					125			
Arg	Ser	Phe	Asp	Asn	Val	Arg	Gln	Gly	Asp	Glu	Leu	Asp	Val	Pro	Ala
			130			135					140				
Gln	Val	Ser	Glu	Lys	Lys	Leu	Thr	Pro	Pro	Pro	Gly	Asn	Ser	Ser	Asp
145					150					155					160
Asn	Leu	Glu	Gln	Gln	Ile	Ala	Ser	Thr	Ser	Gln	Gln	Ile	Gly	Ser	Leu
				165					170					175	
Leu	Ala	Glu	Asp	Met	Asn	Ser	Glu	Gln	Ala	Ala	Asn	Met	Ala	Arg	Gly
			180					185					190		
Trp	Ala	Ser	Ser	Gln	Ala	Ser	Gly	Ala	Met	Thr	Asp	Trp	Leu	Ser	Arg
			195				200					205			
Phe	Gly	Thr	Ala	Arg	Ile	Thr	Leu	Gly	Val	Asp	Glu	Asp	Phe	Ser	Leu
			210			215					220				
Lys	Asn	Ser	Gln	Phe	Asp	Phe	Leu	His	Pro	Trp	Tyr	Glu	Thr	Pro	Asp
225					230					235					240
Asn	Leu	Phe	Phe	Ser	Gln	His	Thr	Leu	His	Arg	Thr	Asp	Glu	Arg	Thr
				245					250					255	
Gln	Ile	Asn	Asn	Gly	Leu	Gly	Trp	Arg	His	Phe	Thr	Pro	Thr	Trp	Met
			260					265					270		
Ser	Gly	Ile	Asn	Phe	Phe	Phe	Asp	His	Asp	Leu	Ser	Arg	Tyr	His	Ser
			275				280					285			
Arg	Ala	Gly	Ile	Gly	Ala	Glu	Tyr	Trp	Arg	Asp	Tyr	Leu	Lys	Leu	Ser
			290			295					300				
Ser	Asn	Gly	Tyr	Leu	Arg	Leu	Thr	Asn	Trp	Arg	Ser	Ala	Pro	Glu	Leu
305					310					315					320
Asp	Asn	Asp	Tyr	Glu	Ala	Arg	Pro	Ala	Asn	Gly	Trp	Asp	Val	Arg	Ala
				325					330					335	
Glu	Ser	Trp	Leu	Pro	Ala	Trp	Pro	His	Leu	Gly	Gly	Lys	Leu	Val	Tyr
			340					345					350		
Glu	Gln	Tyr	Tyr	Gly	Asp	Glu	Val	Ala	Leu	Phe	Asp	Lys	Asp	Asp	Arg
			355				360					365			
Gln	Ser	Asn	Pro	His	Ala	Ile	Thr	Ala	Gly	Leu	Asn	Tyr	Thr	Pro	Phe
			370			375					380				
Pro	Leu	Met	Thr	Phe	Ser	Ala	Glu	Gln	Arg	Gln	Gly	Lys	Gln	Gly	Glu
385					390					395					400
Asn	Asp	Thr	Arg	Phe	Ala	Val	Asp	Phe	Thr	Trp	Gln	Pro	Gly	Ser	Ala
				405					410					415	
Met	Gln	Lys	Gln	Leu	Asp	Pro	Asn	Glu	Val	Ala	Ala	Arg	Arg	Ser	Leu
			420					425					430		
Ala	Gly	Ser	Arg	Tyr	Asp	Leu	Val	Asp	Arg	Asn	Asn	Asn	Ile	Val	Leu

Leu	Leu	Asn	Asp	Val	Met	Val	Thr	Phe	Asn	Val	Asn	Ser	Ala	Glu	Ala		
			900					905					910				
Lys	Leu	Ser	Gln	Thr	Glu	Val	Asn	Ser	His	Asp	Gly	Ile	Ala	Thr	Ala		
			915					920					925				
Thr	Leu	Thr	Ser	Leu	Lys	Asn	Gly	Asp	Tyr	Arg	Val	Thr	Ala	Ser	Val		
			930					935					940				
Ser	Ser	Gly	Ser	Gln	Ala	Asn	Gln	Gln	Val	Asn	Phe	Ile	Gly	Asp	Gln		
945					950					955					960		
Ser	Thr	Ala	Ala	Leu	Thr	Leu	Ser	Val	Pro	Ser	Gly	Asp	Ile	Thr	Val		
				965					970					975			
Thr	Asn	Thr	Ala	Pro	Gln	Tyr	Met	Thr	Ala	Thr	Leu	Gln	Asp	Lys	Asn		
			980						985					990			
Gly	Asn	Pro	Leu	Lys	Asp	Lys	Glu	Ile	Thr	Phe	Ser	Val	Pro	Asn	Asp		
		995					1000						1005				
Val	Ala	Ser	Lys	Phe	Ser	Ile	Ser	Asn	Gly	Gly	Lys	Gly	Met	Thr	Asp		
	1010					1015						1020					
Ser	Asn	Gly	Val	Ala	Ile	Ala	Ser	Leu	Thr	Gly	Thr	Leu	Ala	Gly	Thr		
1025					1030					1035					1040		
His	Met	Ile	Met	Ala	Arg	Leu	Ala	Asn	Ser	Asn	Val	Ser	Asp	Ala	Gln		
				1045					1050					1055			
Pro	Met	Thr	Phe	Val	Ala	Asp	Lys	Asp	Arg	Ala	Val	Val	Val	Leu	Gln		
			1060					1065						1070			
Thr	Ser	Lys	Ala	Glu	Ile	Ile	Gly	Asn	Gly	Val	Asp	Glu	Thr	Thr	Leu		
		1075					1080						1085				
Thr	Ala	Thr	Val	Lys	Asp	Pro	Ser	Asn	His	Pro	Val	Ala	Gly	Ile	Thr		
	1090				1095							1100					
Val	Asn	Phe	Thr	Met	Pro	Gln	Asp	Val	Ala	Ala	Asn	Phe	Thr	Leu	Glu		
1105					1110					1115					1120		
Asn	Asn	Gly	Ile	Ala	Ile	Thr	Gln	Ala	Asn	Gly	Glu	Ala	His	Val	Thr		
			1125					1130						1135			
Leu	Lys	Gly	Lys	Lys	Ala	Gly	Thr	His	Thr	Val	Thr	Ala	Thr	Leu	Gly		
		1140						1145						1150			
Asn	Asn	Asn	Thr	Ser	Asp	Ser	Gln	Pro	Val	Thr	Phe	Val	Ala	Asp	Lys		
		1155					1160						1165				
Ala	Ser	Ala	Gln	Val	Val	Leu	Gln	Ile	Ser	Lys	Asp	Glu	Ile	Thr	Gly		
	1170					1175					1180						
Asn	Gly	Val	Asp	Ser	Ala	Thr	Leu	Thr	Ala	Thr	Val	Lys	Asp	Gln	Phe		
1185					1190					1195					1200		
Asp	Asn	Glu	Val	Asn	Asn	Leu	Pro	Val	Thr	Phe	Ser	Ser	Ala	Ser	Ser		
				1205					1210					1215			
Gly	Leu	Thr	Leu	Thr	Pro	Gly	Val	Ser	Asn	Thr	Asn	Glu	Ser	Gly	Ile		
		1220					1225						1230				
Ala	Gln	Ala	Thr	Leu	Ala	Gly	Val	Ala	Phe	Gly	Glu	Lys	Thr	Val	Thr		
		1235					1240						1245				
Ala	Ser	Leu	Ala	Asn	Asn	Gly	Ala	Ser	Asp	Asn	Lys	Thr	Val	His	Phe		
	1250				1255						1260						
Ile	Gly	Asp	Thr	Ala	Ala	Ala	Lys	Ile	Ile	Glu	Leu	Ala	Pro	Val	Pro		
1265					1270					1275					1280		
Asp	Ser	Ile	Ile	Ala	Gly	Thr	Pro	Gln	Asn	Ser	Ser	Gly	Ser	Val	Ile		
			1285					1290						1295			
Thr	Ala	Thr	Val	Val	Asp	Asn	Asn	Gly	Phe	Pro	Val	Lys	Gly	Val	Thr		
		1300						1305						1310			
Val	Asn	Phe	Thr	Ser	Asn	Ala	Ala	Thr	Ala	Glu	Met	Thr	Asn	Gly	Gly		
	1315					1320							1325				
Gln	Ala	Val	Thr	Asn	Glu	Gln	Gly	Lys	Ala	Thr	Val	Thr	Tyr	Thr	Asn		
	1330					1335					1340						
Thr	Arg	Ser	Ser	Ile	Glu	Ser	Gly	Ala	Arg	Pro	Asp	Thr	Val	Glu	Ala		

1345		1350		1355		1360
Ser Leu Glu Asn Gly	Ser Ser Thr Leu Ser Thr Ser Ile Asn Val Asn					
	1365		1370		1375	
Ala Asp Ala Ser Thr Ala His Leu Thr Leu Leu Gln Ala Leu Phe Asp						
	1380		1385		1390	
Thr Val Ser Ala Gly Glu Thr Thr Ser Leu Tyr Ile Glu Val Lys Asp						
	1395		1400		1405	
Asn Tyr Gly Asn Gly Val Pro Gln Gln Glu Val Thr Leu Ser Val Ser						
	1410		1415		1420	
Pro Ser Glu Gly Val Thr Pro Ser Asn Asn Ala Ile Tyr Thr Thr Asn						
1425	1430		1435		1440	
His Asp Gly Asn Phe Tyr Ala Ser Phe Thr Ala Thr Lys Ala Gly Val						
	1445		1450		1455	
Tyr Gln Leu Thr Ala Thr Leu Glu Asn Gly Asp Ser Met Gln Gln Thr						
	1460		1465		1470	
Val Thr Tyr Val Pro Asn Val Ala Asn Ala Glu Ile Thr Leu Ala Ala						
	1475		1480		1485	
Ser Lys Asp Pro Val Ile Ala Asp Asn Asn Asp Leu Thr Thr Leu Thr						
	1490		1495		1500	
Ala Thr Val Ala Asp Thr Glu Gly Asn Ala Ile Ala Asn Thr Glu Val						
1505	1510		1515		1520	
Thr Phe Thr Leu Pro Glu Asp Val Lys Ala Asn Phe Thr Leu Ser Asp						
	1525		1530		1535	
Gly Gly Lys Val Ile Thr Asp Ala Glu Gly Lys Ala Lys Val Thr Leu						
	1540		1545		1550	
Lys Gly Thr Lys Ala Gly Ala His Thr Val Thr Ala Ser Met Thr Gly						
	1555		1560		1565	
Gly Lys Ser Glu Gln Leu Val Val Asn Phe Ile Ala Asp Thr Leu Thr						
	1570		1575		1580	
Ala Gln Val Asn Leu Asn Val Thr Glu Asp Asn Phe Ile Ala Asn Asn						
1585	1590		1595		1600	
Val Gly Met Thr Arg Leu Gln Ala Thr Val Thr Asp Gly Asn Gly Asn						
	1605		1610		1615	
Pro Leu Ala Asn Glu Ala Val Thr Phe Thr Leu Pro Ala Asp Val Ser						
	1620		1625		1630	
Ala Ser Phe Thr Leu Gly Gln Gly Gly Ser Ala Ile Thr Asp Ile Asn						
	1635		1640		1645	
Gly Lys Ala Glu Val Thr Leu Ser Gly Thr Lys Ser Gly Thr Tyr Pro						
	1650		1655		1660	
Val Thr Val Ser Val Asn Asn Tyr Gly Val Ser Asp Thr Lys Gln Val						
1665	1670		1675		1680	
Thr Leu Ile Ala Asp Ala Gly Thr Ala Lys Leu Ala Ser Leu Thr Ser						
	1685		1690		1695	
Val Tyr Ser Phe Val Val Ser Thr Thr Glu Gly Ala Thr Met Thr Ala						
	1700		1705		1710	
Ser Val Thr Asp Ala Asn Gly Asn Pro Val Glu Gly Ile Lys Val Asn						
	1715		1720		1725	
Phe Arg Gly Thr Ser Val Thr Leu Ser Ser Thr Ser Val Glu Thr Asp						
	1730		1735		1740	
Asp Arg Gly Phe Ala Glu Ile Leu Val Thr Ser Thr Glu Val Gly Leu						
1745	1750		1755		1760	
Lys Thr Val Ser Ala Ser Leu Ala Asp Lys Pro Thr Glu Val Ile Ser						
	1765		1770		1775	
Arg Leu Leu Asn Ala Ser Ala Asp Val Asn Ser Ala Thr Ile Thr Ser						
	1780		1785		1790	
Leu Glu Ile Pro Glu Gly Gln Val Met Val Ala Gln Asp Val Ala Val						
	1795		1800		1805	

Lys Ala His Val Asn Asp Gln Phe Gly Asn Pro Val Ala His Gln Pro
 1810 1815 1820
 Val Thr Phe Ser Ala Glu Pro Ser Ser Gln Met Ile Ile Ser Gln Asn
 1825 1830 1835 1840
 Thr Val Ser Thr Asn Thr Gln Gly Val Ala Glu Val Thr Met Thr Pro
 1845 1850 1855
 Glu Arg Asn Gly Ser Tyr Met Val Lys Ala Ser Leu Pro Asn Gly Ala
 1860 1865 1870
 Ser Leu Glu Lys Gln Leu Glu Ala Ile Asp Glu Lys Leu Thr Leu Thr
 1875 1880 1885
 Ala Ser Ser Pro Leu Ile Gly Val Tyr Ala Pro Thr Gly Ala Thr Leu
 1890 1895 1900
 Thr Ala Thr Leu Thr Ser Ala Asn Gly Thr Pro Val Glu Gly Gln Val
 1905 1910 1915 1920
 Ile Asn Phe Ser Val Thr Pro Glu Gly Ala Thr Leu Ser Gly Gly Lys
 1925 1930 1935
 Val Arg Thr Asn Ser Ser Gly Gln Ala Pro Val Val Leu Thr Ser Asn
 1940 1945 1950
 Lys Val Gly Thr Tyr Thr Val Thr Ala Ser Phe His Asn Gly Val Thr
 1955 1960 1965
 Ile Gln Thr Gln Thr Thr Val Lys Val Thr Gly Asn Ser Ser Thr Ala
 1970 1975 1980
 His Val Ala Ser Phe Ile Ala Asp Pro Ser Thr Ile Ala Ala Thr Asn
 1985 1990 1995 2000
 Thr Asp Leu Ser Thr Leu Lys Ala Thr Val Glu Asp Gly Ser Gly Asn
 2005 2010 2015
 Leu Ile Glu Gly Leu Thr Val Tyr Phe Ala Leu Lys Ser Gly Ser Ala
 2020 2025 2030
 Thr Leu Thr Ser Leu Thr Ala Val Thr Asp Gln Asn Gly Ile Ala Thr
 2035 2040 2045
 Thr Ser Val Lys Gly Ala Met Thr Gly Ser Val Thr Val Ser Ala Val
 2050 2055 2060
 Thr Thr Ala Gly Gly Met Gln Thr Val Asp Ile Thr Leu Val Ala Gly
 2065 2070 2075 2080
 Pro Ala Asp Thr Ser Gln Ser Val Leu Lys Ser Asn Arg Ser Ser Leu
 2085 2090 2095
 Lys Gly Asp Tyr Thr Asp Ser Ala Glu Leu Arg Leu Val Leu His Asp
 2100 2105 2110
 Ile Ser Gly Asn Pro Ile Lys Val Ser Glu Gly Met Glu Phe Val Gln
 2115 2120 2125
 Ser Gly Thr Asn Val Pro Tyr Ile Lys Ile Ser Ala Ile Asp Tyr Ser
 2130 2135 2140
 Leu Asn Ile Asn Gly Asp Tyr Lys Ala Thr Val Thr Gly Gly Gly Glu
 2145 2150 2155 2160
 Gly Ile Ala Thr Leu Ile Pro Val Leu Asn Gly Val His Gln Ala Gly
 2165 2170 2175
 Leu Ser Thr Thr Ile Gln Phe Thr Arg Ala Glu Asp Lys Ile Met Ser
 2180 2185 2190
 Gly Thr Val Ser Val Asn Gly Thr Asp Leu Pro Thr Thr Thr Phe Pro
 2195 2200 2205
 Ser Gln Gly Phe Thr Gly Ala Tyr Tyr Gln Leu Asn Asn Asp Asn Phe
 2210 2215 2220
 Ala Pro Gly Lys Thr Ala Ala Asp Tyr Glu Phe Ser Ser Ser Ala Ser
 2225 2230 2235 2240
 Trp Val Asp Val Asp Ala Thr Gly Lys Val Thr Phe Lys Asn Val Gly
 2245 2250 2255
 Ser Asn Ser Glu Arg Ile Thr Ala Thr Pro Lys Ser Gly Gly Pro Ser

Asn	Gly	Ile	Thr	Ser	Ser	Val	Glu	Gly	Val	Glu	Thr	Asp	Ile	Asn	Ala
145					150					155					160
Ser	Lys	Thr	Arg	Gln	Gln	Leu	Asn	Asp	Val	Ala	Gly	Lys	Met	Lys	Ile
				165					170						175
Ile	Glu	Ala	Arg	Leu	Ser	Ala	Leu	Thr	Asn	Asn	Gln	Thr	Lys	Ser	Leu
			180					185					190		
Lys	Leu	Lys	Pro	Val	Ala	Leu	Pro	Lys	Val	Ala	Ser	Gln	Leu	Pro	Asp
		195					200					205			
Glu	Leu	Gly	Tyr	Ser	Leu	Leu	Ala	Arg	Arg	Ala	Asp	Leu	Gln	Ala	Ala
	210					215					220				
His	Trp	Tyr	Val	Glu	Ser	Ser	Leu	Ser	Thr	Ile	Asp	Ala	Ala	Lys	Ala
225					230					235					240
Ala	Phe	Tyr	Pro	Asp	Ile	Asn	Leu	Met	Ala	Phe	Leu	Gln	Gln	Asp	Ala
				245					250					255	
Leu	His	Leu	Ser	Asp	Leu	Phe	Arg	His	Ser	Ala	Gln	Gln	Met	Gly	Val
			260					265					270		
Thr	Ala	Gly	Leu	Thr	Leu	Pro	Ile	Phe	Asp	Ser	Gly	Arg	Leu	Asn	Ala
		275					280					285			
Asn	Leu	Asp	Ile	Ala	Lys	Ala	Glu	Ser	Asn	Leu	Ser	Ile	Ala	Ser	Tyr
	290					295					300				
Asn	Lys	Ala	Val	Val	Glu	Ala	Val	Asn	Asp	Val	Ala	Arg	Ala	Ala	Ser
305					310					315					320
Gln	Val	Gln	Thr	Leu	Ala	Glu	Lys	Asn	Gln	His	Gln	Ala	Gln	Ile	Glu
				325					330					335	
Arg	Asp	Ala	Leu	Arg	Val	Val	Gly	Leu	Ala	Gln	Ala	Arg	Phe	Asn	Ala
			340					345					350		
Gly	Ile	Ile	Ala	Gly	Ser	Arg	Val	Ser	Glu	Ala	Arg	Ile	Pro	Ala	Leu
		355					360					365			
Arg	Glu	Arg	Ala	Asn	Gly	Leu	Leu	Leu	Gln	Gly	Gln	Trp	Leu	Asp	Ala
	370				375						380				
Ser	Ile	Gln	Leu	Thr	Gly	Ala	Leu	Gly	Gly	Gly	Tyr	Lys	Arg		
385					390					395					

<210> 305
 <211> 96
 <212> PRT
 <213> E. Coli

<400> 305

Met	Tyr	Cys	His	Ala	Lys	Leu	Lys	Asn	Ile	Ser	Gln	His	Thr	Val	Ile
1				5					10					15	
Ser	Ala	His	Leu	Phe	Leu	Pro	Asp	Tyr	Ser	Pro	Met	Asn	Arg	Asp	Ser
			20					25					30		
Phe	Tyr	Pro	Ala	Ile	Ala	Cys	Phe	Pro	Leu	Leu	Leu	Met	Leu	Ala	Gly
		35					40					45			
Cys	Ala	Pro	Met	His	Glu	Thr	Arg	Gln	Ala	Leu	Ser	Gln	Gln	Thr	Pro
	50					55					60				
Ala	Ala	Gln	Val	Asp	Thr	Ala	Leu	Pro	Thr	Ala	Leu	Lys	Met	Val	Gly
65					70					75					80
Gln	Thr	Ala	Asn	Gly	Gly	Trp	Ser	Ile	Thr	Ile	Ile	Asn	Ser	Leu	Pro
			85						90					95	

<210> 306
 <211> 315
 <212> PRT

<213> E. Coli

<400> 306

Met Arg Val Leu Leu Ala Pro Met Glu Gly Val Leu Asp Ser Leu Val
1 5 10 15
Arg Glu Leu Leu Thr Glu Val Asn Asp Tyr Asp Leu Cys Ile Thr Glu
20 25 30
Phe Val Arg Val Val Asp Gln Leu Leu Pro Val Lys Val Phe His Arg
35 40 45
Ile Cys Pro Glu Leu Gln Asn Ala Ser Arg Thr Pro Ser Gly Thr Leu
50 55 60
Val Arg Val Gln Leu Leu Gly Gln Phe Pro Gln Trp Leu Ala Glu Asn
65 70 75 80
Ala Ala Arg Ala Val Glu Leu Gly Ser Trp Gly Val Asp Leu Asn Cys
85 90 95
Gly Cys Pro Ser Lys Thr Val Asn Gly Ser Gly Gly Gly Ala Thr Leu
100 105 110
Leu Lys Asp Pro Glu Leu Ile Tyr Gln Gly Ala Lys Ala Met Arg Glu
115 120 125
Ala Val Pro Ala His Leu Pro Val Ser Val Lys Val Arg Leu Gly Trp
130 135 140
Asp Ser Gly Glu Lys Lys Phe Glu Ile Ala Asp Ala Val Gln Gln Ala
145 150 155 160
Gly Ala Thr Glu Leu Val Val His Gly Arg Thr Lys Glu Gln Gly Tyr
165 170 175
Arg Ala Glu His Ile Asp Trp Gln Ala Ile Gly Asp Ile Arg Gln Arg
180 185 190
Leu Asn Ile Pro Val Ile Ala Asn Gly Glu Ile Trp Asp Trp Gln Ser
195 200 205
Ala Gln Gln Cys Met Ala Ile Ser Gly Cys Asp Ala Val Met Ile Gly
210 215 220
Arg Gly Ala Leu Asn Ile Pro Asn Leu Ser Arg Val Val Lys Tyr Asn
225 230 235 240
Glu Pro Arg Met Pro Trp Pro Glu Val Val Ala Leu Leu Gln Lys Tyr
245 250 255
Thr Arg Leu Glu Lys Gln Gly Asp Thr Gly Leu Tyr His Val Ala Arg
260 265 270
Ile Lys Gln Trp Leu Ser Tyr Leu Arg Lys Glu Tyr Asp Glu Ala Thr
275 280 285
Glu Leu Phe Gln His Val Arg Val Leu Asn Asn Ser Pro Asp Ile Ala
290 295 300
Arg Ala Ile Gln Ala Ile Asp Ile Glu Lys Leu
305 310 315

<210> 307

<211> 296

<212> PRT

<213> E. Coli

<400> 307

Met Thr Ile Ser Thr Thr Ser Thr Pro His Asp Ala Val Phe Lys Ser
1 5 10 15
Phe Leu Arg His Pro Asp Thr Ala Arg Asp Phe Ile Asp Ile His Leu
20 25 30
Pro Ala Pro Leu Arg Lys Leu Cys Asp Leu Thr Thr Leu Lys Leu Glu
35 40 45

Pro	Asn	Ser	Phe	Ile	Asp	Glu	Asp	Leu	Arg	Gln	Tyr	Tyr	Ser	Asp	Leu
50						55					60				
Leu	Trp	Ser	Val	Lys	Thr	Gln	Glu	Gly	Val	Gly	Tyr	Ile	Tyr	Val	Val
65					70					75					80
Ile	Glu	His	Gln	Ser	Lys	Pro	Glu	Glu	Leu	Met	Ala	Phe	Arg	Met	Met
			85						90					95	
Arg	Tyr	Ser	Ile	Ala	Ala	Met	Gln	Asn	His	Leu	Asp	Ala	Gly	Tyr	Lys
			100					105					110		
Glu	Leu	Pro	Leu	Val	Leu	Pro	Met	Leu	Phe	Tyr	His	Gly	Cys	Arg	Ser
		115					120					125			
Pro	Tyr	Pro	Tyr	Ser	Leu	Cys	Trp	Leu	Asp	Glu	Phe	Ala	Glu	Pro	Ala
		130				135					140				
Ile	Ala	Arg	Lys	Ile	Tyr	Ser	Ser	Ala	Phe	Pro	Leu	Val	Asp	Ile	Thr
145					150					155					160
Val	Val	Pro	Asp	Asp	Glu	Ile	Met	Gln	His	Arg	Lys	Met	Ala	Leu	Leu
				165					170					175	
Glu	Leu	Ile	Gln	Lys	His	Ile	Arg	Gln	Arg	Asp	Leu	Leu	Gly	Leu	Val
			180					185					190		
Asp	Gln	Ile	Val	Ser	Leu	Leu	Val	Thr	Gly	Asn	Thr	Asn	Asp	Arg	Gln
			195				200					205			
Leu	Lys	Ala	Leu	Phe	Asn	Tyr	Val	Leu	Gln	Thr	Gly	Asp	Ala	Gln	Arg
			210			215					220				
Phe	Arg	Ala	Phe	Ile	Gly	Glu	Ile	Ala	Glu	Arg	Ala	Pro	Gln	Glu	Lys
225					230					235					240
Glu	Lys	Leu	Met	Thr	Ile	Ala	Asp	Arg	Leu	Arg	Glu	Glu	Gly	Ala	Met
				245					250					255	
Gln	Gly	Lys	His	Glu	Glu	Ala	Leu	Arg	Ile	Ala	Gln	Glu	Met	Leu	Asp
			260					265					270		
Arg	Gly	Leu	Asp	Arg	Glu	Leu	Val	Met	Met	Val	Thr	Arg	Leu	Ser	Pro
		275					280					285			
Asp	Asp	Leu	Ile	Ala	Gln	Ser	His								
		290				295									

<210> 308

<211> 555

<212> PRT

<213> E. Coli

<400> 308

Met	Ala	Gln	Phe	Val	Tyr	Thr	Met	His	Arg	Val	Gly	Lys	Val	Val	Pro
1				5					10					15	
Pro	Lys	Arg	His	Ile	Leu	Lys	Asn	Ile	Ser	Leu	Ser	Phe	Phe	Pro	Gly
			20					25					30		
Ala	Lys	Ile	Gly	Val	Leu	Gly	Leu	Asn	Gly	Ala	Gly	Lys	Ser	Thr	Leu
			35				40					45			
Leu	Arg	Ile	Met	Ala	Gly	Ile	Asp	Lys	Asp	Ile	Glu	Gly	Glu	Ala	Arg
	50					55				60					
Pro	Gln	Pro	Asp	Ile	Lys	Ile	Gly	Tyr	Leu	Pro	Gln	Glu	Pro	Gln	Leu
65					70					75					80
Asn	Pro	Glu	His	Thr	Val	Arg	Glu	Ser	Ile	Glu	Glu	Ala	Val	Ser	Glu
			85						90					95	
Val	Val	Asn	Ala	Leu	Lys	Arg	Leu	Asp	Glu	Val	Tyr	Ala	Leu	Tyr	Ala
			100					105					110		
Asp	Pro	Asp	Ala	Asp	Phe	Asp	Lys	Leu	Ala	Ala	Glu	Gln	Gly	Arg	Leu
		115					120					125			
Glu	Glu	Ile	Ile	Gln	Ala	His	Asp	Gly	His	Asn	Leu	Asn	Val	Gln	Leu

130 135 140
 145 150 155 160
 165 170 175
 180 185 190
 195 200 205
 210 215 220
 225 230 235 240
 245 250 255
 260 265 270
 275 280 285
 290 295 300
 305 310 315 320
 325 330 335
 340 345 350
 355 360 365
 370 375 380
 385 390 395 400
 405 410 415
 420 425 430
 435 440 445
 450 455 460
 465 470 475 480
 485 490 495
 500 505 510
 515 520 525
 530 535 540
 545 550 555

Glu Arg Ala Ala Asp Ala Leu Arg Leu Pro Asp Trp Asp Ala Lys Ile
 Ala Asn Leu Ser Gly Gly Glu Arg Arg Arg Val Ala Leu Cys Arg Leu
 Leu Leu Glu Lys Pro Asp Met Leu Leu Leu Asp Glu Pro Thr Asn His
 Leu Asp Ala Glu Ser Val Ala Trp Leu Glu Arg Phe Leu His Asp Phe
 Glu Gly Thr Val Val Ala Ile Thr His Asp Arg Tyr Phe Leu Asp Asn
 Val Ala Gly Trp Ile Leu Glu Leu Asp Arg Gly Glu Gly Ile Pro Trp
 Glu Gly Asn Tyr Ser Ser Trp Leu Glu Gln Lys Asp Gln Arg Leu Ala
 Gln Glu Ala Ser Gln Glu Ala Ala Arg Arg Lys Ser Ile Glu Lys Glu
 Leu Glu Trp Val Arg Gln Gly Thr Lys Gly Arg Gln Ser Lys Gly Lys
 Ala Arg Leu Ala Arg Phe Glu Glu Leu Asn Ser Thr Glu Tyr Gln Lys
 Arg Asn Glu Thr Asn Glu Leu Phe Ile Pro Pro Gly Pro Arg Leu Gly
 Asp Lys Val Leu Glu Val Ser Asn Leu Arg Lys Ser Tyr Gly Asp Arg
 Leu Leu Ile Asp Asp Leu Ser Phe Ser Ile Pro Lys Gly Ala Ile Val
 Gly Ile Ile Gly Pro Asn Gly Ala Gly Lys Ser Thr Leu Phe Arg Met
 Ile Ser Gly Gln Glu Gln Pro Asp Ser Gly Thr Ile Thr Leu Gly Glu
 Thr Val Lys Leu Ala Ser Val Asp Gln Phe Arg Asp Ser Met Asp Asn
 Ser Lys Thr Val Trp Glu Glu Val Ser Gly Gly Leu Asp Ile Met Lys
 Ile Gly Asn Thr Glu Met Pro Ser Arg Ala Tyr Val Gly Arg Phe Asn
 Phe Lys Gly Val Asp Gln Gly Lys Arg Val Gly Glu Leu Ser Gly Gly
 Glu Arg Gly Arg Leu His Leu Ala Lys Leu Leu Gln Val Gly Gly Asn
 Met Leu Leu Leu Asp Glu Pro Thr Asn Asp Leu Asp Ile Glu Thr Leu
 Arg Ala Leu Glu Asn Ala Leu Leu Glu Phe Pro Gly Cys Ala Met Val
 Ile Ser His Asp Arg Trp Phe Leu Asp Arg Ile Ala Thr His Ile Leu
 Asp Tyr Gln Asp Glu Gly Lys Val Glu Phe Phe Glu Gly Asn Phe Thr
 Glu Tyr Glu Glu Tyr Lys Lys Arg Thr Leu Gly Ala Asp Ala Leu Glu
 Pro Lys Arg Ile Lys Tyr Lys Arg Ile Ala Lys

<211> 173
 <212> PRT
 <213> E. Coli

<400> 309

Met	Ser	Lys	Pro	Lys	Tyr	Pro	Phe	Glu	Lys	Arg	Leu	Glu	Val	Val	Asn
1				5					10					15	
His	Tyr	Phe	Thr	Thr	Asp	Asp	Gly	Tyr	Arg	Ile	Ile	Ser	Ala	Arg	Phe
			20					25					30		
Gly	Val	Pro	Arg	Thr	Gln	Val	Arg	Thr	Trp	Val	Ala	Leu	Tyr	Glu	Lys
		35					40					45			
His	Gly	Glu	Lys	Gly	Leu	Ile	Pro	Lys	Pro	Lys	Gly	Val	Ser	Ala	Asp
	50					55					60				
Pro	Glu	Leu	Arg	Ile	Lys	Val	Val	Lys	Ala	Val	Ile	Glu	Gln	His	Met
65					70					75					80
Ser	Leu	Asn	Gln	Ala	Ala	Ala	His	Phe	Met	Leu	Ala	Gly	Ser	Gly	Ser
				85					90					95	
Val	Ala	Arg	Trp	Leu	Lys	Val	Tyr	Glu	Glu	Arg	Gly	Glu	Ala	Gly	Leu
			100						105					110	
Arg	Ala	Leu	Lys	Ile	Gly	Thr	Lys	Arg	Asn	Ile	Ala	Ile	Ser	Val	Asp
		115					120						125		
Pro	Glu	Lys	Ala	Ala	Ser	Ala	Leu	Glu	Leu	Ser	Lys	Asp	Arg	Arg	Ile
	130					135					140				
Glu	Asp	Leu	Glu	Arg	Gln	Val	Arg	Phe	Leu	Glu	Thr	Arg	Leu	Met	Tyr
145					150					155					160
Leu	Lys	Lys	Leu	Lys	Ala	Leu	Ala	His	Pro	Thr	Lys	Lys			
				165					170						

<210> 310
 <211> 283
 <212> PRT
 <213> E. Coli

<400> 310

Met	Lys	Val	Leu	Asn	Glu	Leu	Arg	Gln	Phe	Tyr	Pro	Leu	Asp	Glu	Leu
1				5					10					15	
Leu	Arg	Ala	Ala	Glu	Ile	Pro	Arg	Ser	Thr	Phe	Tyr	Tyr	His	Leu	Lys
			20					25					30		
Ala	Leu	Ser	Lys	Pro	Asp	Lys	Tyr	Ala	Asp	Val	Lys	Lys	Arg	Ile	Ser
		35					40					45			
Glu	Ile	Tyr	His	Glu	Asn	Arg	Gly	Arg	Tyr	Gly	Tyr	Arg	Arg	Val	Thr
	50					55					60				
Leu	Ser	Leu	His	Arg	Glu	Gly	Lys	Gln	Ile	Asn	His	Lys	Ala	Val	Gln
65					70					75					80
Arg	Leu	Met	Gly	Thr	Leu	Ser	Leu	Lys	Ala	Ala	Ile	Lys	Val	Lys	Arg
			85						90					95	
Tyr	Arg	Ser	Tyr	Arg	Gly	Glu	Val	Gly	Gln	Thr	Ala	Pro	Asn	Val	Leu
		100						105					110		
Gln	Arg	Asp	Phe	Lys	Ala	Thr	Arg	Pro	Asn	Glu	Lys	Trp	Val	Thr	Asp
		115					120					125			
Val	Thr	Glu	Phe	Ala	Val	Asn	Gly	Arg	Lys	Leu	Tyr	Leu	Ser	Pro	Val
	130					135					140				
Ile	Asp	Leu	Phe	Asn	Asn	Glu	Val	Ile	Ser	Tyr	Ser	Leu	Ser	Glu	Arg
145					150					155					160
Pro	Val	Met	Asn	Met	Val	Glu	Asn	Met	Leu	Asp	Gln	Ala	Phe	Lys	Lys
				165					170					175	

Leu	Asn	Pro	His	Glu	His	Pro	Val	Leu	His	Ser	Asp	Gln	Gly	Trp	Gln
			180					185					190		
Tyr	Arg	Met	Arg	Arg	Tyr	Gln	Asn	Ile	Leu	Lys	Glu	His	Gly	Ile	Lys
		195					200					205			
Gln	Ser	Met	Ser	Arg	Lys	Gly	Asn	Cys	Leu	Asp	Asn	Ala	Val	Val	Glu
		210				215					220				
Cys	Phe	Phe	Gly	Thr	Leu	Lys	Ser	Glu	Cys	Phe	Tyr	Leu	Asp	Glu	Phe
225					230					235					240
Ser	Asn	Ile	Ser	Glu	Leu	Lys	Asp	Ala	Val	Thr	Glu	Tyr	Ile	Glu	Tyr
			245						250					255	
Tyr	Asn	Ser	Arg	Arg	Ile	Ser	Leu	Lys	Leu	Lys	Gly	Leu	Thr	Pro	Ile
			260					265						270	
Glu	Tyr	Arg	Asn	Gln	Thr	Tyr	Met	Pro	Arg	Val					
		275					280								

<210> 311

<211> 38

<212> PRT

<213> E. Coli

<400> 311

Met	Lys	Val	Arg	Ala	Ser	Val	Lys	Lys	Leu	Cys	Arg	Asn	Cys	Lys	Ile
1				5					10					15	
Val	Lys	Arg	Asp	Gly	Val	Ile	Arg	Val	Ile	Cys	Ser	Ala	Glu	Pro	Lys
			20					25					30		
His	Lys	Gln	Arg	Gln	Gly										
			35												

<210> 312

<211> 443

<212> PRT

<213> E. Coli

<400> 312

Met	Ala	Lys	Gln	Pro	Gly	Leu	Asp	Phe	Gln	Ser	Ala	Lys	Gly	Gly	Leu
1				5					10					15	
Gly	Glu	Leu	Lys	Arg	Arg	Leu	Leu	Phe	Val	Ile	Gly	Ala	Leu	Ile	Val
			20					25					30		
Phe	Arg	Ile	Gly	Ser	Phe	Ile	Pro	Ile	Pro	Gly	Ile	Asp	Ala	Ala	Val
		35					40					45			
Leu	Ala	Lys	Leu	Leu	Glu	Gln	Gln	Arg	Gly	Thr	Ile	Ile	Glu	Met	Phe
		50				55					60				
Asn	Met	Phe	Ser	Gly	Gly	Ala	Leu	Ser	Arg	Ala	Ser	Ile	Phe	Ala	Leu
65				70					75						80
Gly	Ile	Met	Pro	Tyr	Ile	Ser	Ala	Ser	Ile	Ile	Ile	Gln	Leu	Leu	Thr
			85						90					95	
Val	Val	His	Pro	Thr	Leu	Ala	Glu	Ile	Lys	Lys	Glu	Gly	Glu	Ser	Gly
			100					105					110		
Arg	Arg	Lys	Ile	Ser	Gln	Tyr	Thr	Arg	Tyr	Gly	Thr	Leu	Val	Leu	Ala
		115					120					125			
Ile	Phe	Gln	Ser	Ile	Gly	Ile	Ala	Thr	Gly	Leu	Pro	Asn	Met	Pro	Gly
		130				135					140				
Met	Gln	Gly	Leu	Val	Ile	Asn	Pro	Gly	Phe	Ala	Phe	Tyr	Phe	Thr	Ala
145					150					155					160
Val	Val	Ser	Leu	Val	Thr	Gly	Thr	Met	Phe	Leu	Met	Trp	Leu	Gly	Glu
				165					170					175	

Gln Ile Thr Glu Arg Gly Ile Gly Asn Gly Ile Ser Ile Ile Ile Phe
 180 185 190
 Ala Gly Ile Val Ala Gly Leu Pro Pro Ala Ile Ala His Thr Ile Glu
 195 200 205
 Gln Ala Arg Gln Gly Asp Leu His Phe Leu Val Leu Leu Leu Val Ala
 210 215 220
 Val Leu Val Phe Ala Val Thr Phe Phe Val Val Phe Val Glu Arg Gly
 225 230 235 240
 Gln Arg Arg Ile Val Val Asn Tyr Ala Lys Arg Gln Gln Gly Arg Arg
 245 250 255
 Val Tyr Ala Ala Gln Ser Thr His Leu Pro Leu Lys Val Asn Met Ala
 260 265 270
 Gly Val Ile Pro Ala Ile Phe Ala Ser Ser Ile Ile Leu Phe Pro Ala
 275 280 285
 Thr Ile Ala Ser Trp Phe Gly Gly Gly Thr Gly Trp Asn Trp Leu Thr
 290 295 300
 Thr Ile Ser Leu Tyr Leu Gln Pro Gly Gln Pro Leu Tyr Val Leu Leu
 305 310 315 320
 Tyr Ala Ser Ala Ile Ile Phe Phe Cys Phe Phe Tyr Thr Ala Leu Val
 325 330 335
 Phe Asn Pro Arg Glu Thr Ala Asp Asn Leu Lys Lys Ser Gly Ala Phe
 340 345 350
 Val Pro Gly Ile Arg Pro Gly Glu Gln Thr Ala Lys Tyr Ile Asp Lys
 355 360 365
 Val Met Thr Arg Leu Thr Leu Val Gly Ala Leu Tyr Ile Thr Phe Ile
 370 375 380
 Cys Leu Ile Pro Glu Phe Met Arg Asp Ala Met Lys Val Pro Phe Tyr
 385 390 395 400
 Phe Gly Gly Thr Ser Leu Leu Ile Val Val Val Val Ile Met Asp Phe
 405 410 415
 Met Ala Gln Val Gln Thr Leu Met Met Ser Ser Gln Tyr Glu Ser Ala
 420 425 430
 Leu Lys Lys Ala Asn Leu Lys Gly Tyr Gly Arg
 435 440

<210> 313
 <211> 144
 <212> PRT
 <213> E. Coli

<400> 313
 Met Arg Leu Asn Thr Leu Ser Pro Ala Glu Gly Ser Lys Lys Ala Gly
 1 5 10 15
 Lys Arg Leu Gly Arg Gly Ile Gly Ser Gly Leu Gly Lys Thr Gly Gly
 20 25 30
 Arg Gly His Lys Gly Gln Lys Ser Arg Ser Gly Gly Gly Val Arg Arg
 35 40 45
 Gly Phe Glu Gly Gly Gln Met Pro Leu Tyr Arg Arg Leu Pro Lys Phe
 50 55 60
 Gly Phe Thr Ser Arg Lys Ala Ala Ile Thr Ala Glu Ile Arg Leu Ser
 65 70 75 80
 Asp Leu Ala Lys Val Glu Gly Gly Val Val Asp Leu Asn Thr Leu Lys
 85 90 95
 Ala Ala Asn Ile Ile Gly Ile Gln Ile Glu Phe Ala Lys Val Ile Leu
 100 105 110

Ala	Gly	Glu	Val	Thr	Thr	Pro	Val	Thr	Val	Arg	Gly	Leu	Arg	Val	Thr
	115						120					125			
Lys	Gly	Ala	Arg	Ala	Ala	Ile	Glu	Ala	Ala	Gly	Gly	Lys	Ile	Glu	Glu
	130					135					140				

<210> 314
 <211> 59
 <212> PRT
 <213> E. Coli

<400> 314

Met	Ala	Lys	Thr	Ile	Lys	Ile	Thr	Gln	Thr	Arg	Ser	Ala	Ile	Gly	Arg
1				5					10					15	
Leu	Pro	Lys	His	Lys	Ala	Thr	Leu	Leu	Gly	Leu	Gly	Leu	Arg	Arg	Ile
		20					25					30			
Gly	His	Thr	Val	Glu	Arg	Glu	Asp	Thr	Pro	Ala	Ile	Arg	Gly	Met	Ile
	35					40						45			
Asn	Ala	Val	Ser	Phe	Met	Val	Lys	Val	Glu	Glu					
	50					55									

<210> 315
 <211> 167
 <212> PRT
 <213> E. Coli

<400> 315

Met	Ala	His	Ile	Glu	Lys	Gln	Ala	Gly	Glu	Leu	Gln	Glu	Lys	Leu	Ile
1				5					10					15	
Ala	Val	Asn	Arg	Val	Ser	Lys	Thr	Val	Lys	Gly	Gly	Arg	Ile	Phe	Ser
		20					25					30			
Phe	Thr	Ala	Leu	Thr	Val	Val	Gly	Asp	Gly	Asn	Gly	Arg	Val	Gly	Phe
	35					40					45				
Gly	Tyr	Gly	Lys	Ala	Arg	Glu	Val	Pro	Ala	Ala	Ile	Gln	Lys	Ala	Met
	50					55					60				
Glu	Lys	Ala	Arg	Arg	Asn	Met	Ile	Asn	Val	Ala	Leu	Asn	Asn	Gly	Thr
65					70				75					80	
Leu	Gln	His	Pro	Val	Lys	Gly	Val	His	Thr	Gly	Ser	Arg	Val	Phe	Met
			85					90					95		
Gln	Pro	Ala	Ser	Glu	Gly	Thr	Gly	Ile	Ile	Ala	Gly	Gly	Ala	Met	Arg
		100					105						110		
Ala	Val	Leu	Glu	Val	Ala	Gly	Val	His	Asn	Val	Leu	Ala	Lys	Ala	Tyr
	115					120					125				
Gly	Ser	Thr	Asn	Pro	Ile	Asn	Val	Val	Arg	Ala	Thr	Ile	Asp	Gly	Leu
	130				135					140					
Glu	Asn	Met	Asn	Ser	Pro	Glu	Met	Val	Ala	Ala	Lys	Arg	Gly	Lys	Ser
145				150					155						160
Val	Glu	Glu	Ile	Leu	Gly	Lys									
				165											

<210> 316
 <211> 117
 <212> PRT
 <213> E. Coli

<400> 316

Met	Asp	Lys	Lys	Ser	Ala	Arg	Ile	Arg	Arg	Ala	Thr	Arg	Ala	Arg	Arg
1				5				10						15	
Lys	Leu	Gln	Glu	Leu	Gly	Ala	Thr	Arg	Leu	Val	Val	His	Arg	Thr	Pro
		20						25					30		
Arg	His	Ile	Tyr	Ala	Gln	Val	Ile	Ala	Pro	Asn	Gly	Ser	Glu	Val	Leu
	35					40					45				
Val	Ala	Ala	Ser	Thr	Val	Glu	Lys	Ala	Ile	Ala	Glu	Gln	Leu	Lys	Tyr
	50					55					60				
Thr	Gly	Asn	Lys	Asp	Ala	Ala	Ala	Ala	Val	Gly	Lys	Ala	Val	Ala	Glu
65					70					75					80
Arg	Ala	Leu	Glu	Lys	Gly	Ile	Lys	Asp	Val	Ser	Phe	Asp	Arg	Ser	Gly
			85					90					95		
Phe	Gln	Tyr	His	Gly	Arg	Val	Gln	Ala	Leu	Ala	Asp	Ala	Ala	Arg	Glu
			100					105					110		
Ala	Gly	Leu	Gln	Phe											
			115												

<210> 317

<211> 177

<212> PRT

<213> E. Coli

<400> 317

Met	Ser	Arg	Val	Ala	Lys	Ala	Pro	Val	Val	Val	Pro	Ala	Gly	Val	Asp
1				5				10						15	
Val	Lys	Ile	Asn	Gly	Gln	Val	Ile	Thr	Ile	Lys	Gly	Lys	Asn	Gly	Glu
		20						25					30		
Leu	Thr	Arg	Thr	Leu	Asn	Asp	Ala	Val	Glu	Val	Lys	His	Ala	Asp	Asn
	35					40						45			
Thr	Leu	Thr	Phe	Gly	Pro	Arg	Asp	Gly	Tyr	Ala	Asp	Gly	Trp	Ala	Gln
	50				55						60				
Ala	Gly	Thr	Ala	Arg	Ala	Leu	Leu	Asn	Ser	Met	Val	Ile	Gly	Val	Thr
65					70					75					80
Glu	Gly	Phe	Thr	Lys	Lys	Leu	Gln	Leu	Val	Gly	Val	Gly	Tyr	Arg	Ala
				85				90					95		
Ala	Val	Lys	Gly	Asn	Val	Ile	Asn	Leu	Ser	Leu	Gly	Phe	Ser	His	Pro
			100					105					110		
Val	Asp	His	Gln	Leu	Pro	Ala	Gly	Ile	Thr	Ala	Glu	Cys	Pro	Thr	Gln
	115						120					125			
Thr	Glu	Ile	Val	Leu	Lys	Gly	Ala	Asp	Lys	Gln	Val	Ile	Gly	Gln	Val
	130					135					140				
Ala	Ala	Asp	Leu	Arg	Ala	Tyr	Arg	Arg	Pro	Glu	Pro	Tyr	Lys	Gly	Lys
145					150					155					160
Gly	Val	Arg	Tyr	Ala	Asp	Glu	Val	Val	Arg	Thr	Lys	Glu	Ala	Lys	Lys
				165					170					175	

Lys

<210> 318

<211> 130

<212> PRT

<213> E. Coli

<400> 318

Met	Ser	Met	Gln	Asp	Pro	Ile	Ala	Asp	Met	Leu	Thr	Arg	Ile	Arg	Asn
1				5					10					15	
Gly	Gln	Ala	Ala	Asn	Lys	Ala	Ala	Val	Thr	Met	Pro	Ser	Ser	Lys	Leu
		20						25					30		
Lys	Val	Ala	Ile	Ala	Asn	Val	Leu	Lys	Glu	Glu	Gly	Phe	Ile	Glu	Asp
	35						40					45			
Phe	Lys	Val	Glu	Gly	Asp	Thr	Lys	Pro	Glu	Leu	Glu	Leu	Thr	Leu	Lys
	50					55					60				
Tyr	Phe	Gln	Gly	Lys	Ala	Val	Val	Glu	Ser	Ile	Gln	Arg	Val	Ser	Arg
65					70					75					80
Pro	Gly	Leu	Arg	Ile	Tyr	Lys	Arg	Lys	Asp	Glu	Leu	Pro	Lys	Val	Met
			85						90					95	
Ala	Gly	Leu	Gly	Ile	Ala	Val	Val	Ser	Thr	Ser	Lys	Gly	Val	Met	Thr
		100						105					110		
Asp	Arg	Ala	Ala	Arg	Gln	Ala	Gly	Leu	Gly	Gly	Glu	Ile	Ile	Cys	Tyr
	115						120						125		
Val	Ala														
	130														

<210> 319
 <211> 101
 <212> PRT
 <213> E. Coli

<400> 319

Met	Ala	Lys	Gln	Ser	Met	Lys	Ala	Arg	Glu	Val	Lys	Arg	Val	Ala	Leu
1				5					10					15	
Ala	Asp	Lys	Tyr	Phe	Ala	Lys	Arg	Ala	Glu	Leu	Lys	Ala	Ile	Ile	Ser
		20						25					30		
Asp	Val	Asn	Ala	Ser	Asp	Glu	Asp	Arg	Trp	Asn	Ala	Val	Leu	Lys	Leu
		35					40					45			
Gln	Thr	Leu	Pro	Arg	Asp	Ser	Ser	Pro	Ser	Arg	Gln	Arg	Asn	Arg	Cys
	50					55					60				
Arg	Gln	Thr	Gly	Arg	Pro	His	Gly	Phe	Leu	Arg	Lys	Phe	Gly	Leu	Ser
65					70				75						80
Arg	Ile	Lys	Val	Arg	Glu	Ala	Ala	Met	Arg	Gly	Glu	Ile	Pro	Gly	Leu
				85					90					95	
Lys	Lys	Ala	Ser	Trp											
			100												

<210> 320
 <211> 179
 <212> PRT
 <213> E. Coli

<400> 320

Met	Ala	Lys	Leu	His	Asp	Tyr	Tyr	Lys	Asp	Glu	Val	Val	Lys	Lys	Leu
1				5					10					15	
Met	Thr	Glu	Phe	Asn	Tyr	Asn	Ser	Val	Met	Gln	Val	Pro	Arg	Val	Glu
		20						25					30		
Lys	Ile	Thr	Leu	Asn	Met	Gly	Val	Gly	Glu	Ala	Ile	Ala	Asp	Lys	Lys
	35					40						45			
Leu	Leu	Asp	Asn	Ala	Ala	Ala	Asp	Leu	Ala	Ala	Ile	Ser	Gly	Gln	Lys

50 55 60
 Pro Leu Ile Thr Lys Ala Arg Lys Ser Val Ala Gly Phe Lys Ile Arg
 65 70 75 80
 Gln Gly Tyr Pro Ile Gly Cys Lys Val Thr Leu Arg Gly Glu Arg Met
 85 90 95
 Trp Glu Phe Phe Glu Arg Leu Ile Thr Ile Ala Val Pro Arg Ile Arg
 100 105 110
 Asp Phe Arg Gly Leu Ser Ala Lys Ser Phe Asp Gly Arg Gly Asn Tyr
 115 120 125
 Ser Met Gly Val Arg Glu Gln Ile Ile Phe Pro Glu Ile Asp Tyr Asp
 130 135 140
 Lys Val Asp Arg Val Arg Gly Leu Asp Ile Thr Ile Thr Thr Thr Ala
 145 150 155 160
 Lys Ser Asp Glu Glu Gly Arg Ala Leu Leu Ala Ala Phe Asp Phe Pro
 165 170 175
 Phe Arg Lys

<210> 321Z
 <211> 104
 <212> PRT
 <213> E. Coli

<400> 321
 Met Ala Ala Lys Ile Arg Arg Asp Asp Glu Val Ile Val Leu Thr Gly
 1 5 10 15
 Lys Asp Lys Gly Lys Arg Gly Lys Val Lys Asn Val Leu Ser Ser Gly
 20 25 30
 Lys Val Ile Val Glu Gly Ile Asn Leu Val Lys Lys His Gln Lys Pro
 35 40 45
 Val Pro Ala Leu Asn Gln Pro Gly Gly Ile Val Glu Lys Glu Ala Ala
 50 55 60
 Ile Gln Val Ser Asn Val Ala Ile Phe Asn Ala Ala Thr Gly Lys Ala
 65 70 75 80
 Asp Arg Val Gly Phe Arg Phe Glu Asp Gly Lys Lys Val Arg Phe Phe
 85 90 95
 Lys Ser Asn Ser Glu Thr Ile Lys
 100

<210> 322
 <211> 123
 <212> PRT
 <213> E. Coli

<400> 322
 Met Ile Gln Glu Gln Thr Met Leu Asn Val Ala Asp Asn Ser Gly Ala
 1 5 10 15
 Arg Arg Val Met Cys Ile Lys Val Leu Gly Gly Ser His Arg Arg Tyr
 20 25 30
 Ala Gly Val Gly Asp Ile Ile Lys Ile Thr Ile Lys Glu Ala Ile Pro
 35 40 45
 Arg Gly Lys Val Lys Lys Gly Asp Val Leu Lys Ala Val Val Val Arg
 50 55 60
 Thr Lys Lys Gly Val Arg Arg Pro Asp Gly Ser Val Ile Arg Phe Asp
 65 70 75 80

Gly Asn Ala Cys Val Leu Leu Asn Asn Asn Ser Glu Gln Pro Ile Gly
 85 90 95
 Thr Arg Ile Phe Gly Pro Val Thr Arg Glu Leu Arg Ser Glu Lys Phe
 100 105 110
 Met Lys Ile Ile Ser Leu Ala Pro Glu Val Leu
 115 120

<210> 323
 <211> 188
 <212> PRT
 <213> E. Coli

<400> 323

Met Phe Lys Gly Gln Lys Thr Leu Ala Ala Leu Ala Val Ser Leu Leu
 1 5 10 15
 Phe Thr Ala Pro Val Tyr Ala Ala Asp Glu Gly Ser Gly Glu Ile His
 20 25 30
 Phe Lys Gly Glu Val Ile Glu Ala Pro Cys Glu Ile His Pro Glu Asp
 35 40 45
 Ile Asp Lys Asn Ile Asp Leu Gly Gln Val Thr Thr Thr His Ile Asn
 50 55 60
 Arg Glu His His Ser Asn Lys Val Ala Val Asp Ile Arg Leu Ile Asn
 65 70 75 80
 Cys Asp Leu Pro Ala Ser Asp Asn Gly Ser Gly Met Pro Val Ser Lys
 85 90 95
 Val Gly Val Thr Phe Asp Ser Thr Ala Lys Thr Thr Gly Ala Thr Pro
 100 105 110
 Leu Leu Ser Asn Thr Ser Ala Gly Glu Ala Thr Gly Val Gly Val Arg
 115 120 125
 Leu Met Asp Lys Asn Asp Gly Asn Ile Val Leu Gly Ser Ala Ala Pro
 130 135 140
 Asp Leu Asp Leu Asp Ala Ser Ser Ser Glu Gln Thr Leu Asn Phe Phe
 145 150 155 160
 Ala Trp Met Glu Gln Ile Asp Asn Ala Val Asp Val Thr Ala Gly Glu
 165 170 175
 Val Thr Ala Asn Ala Thr Tyr Val Leu Asp Tyr Lys
 180 185

<210> 324
 <211> 427
 <212> PRT
 <213> E. Coli

<400> 324

Met Ala Asp Thr Lys Ala Lys Leu Thr Leu Asn Gly Asp Thr Ala Val
 1 5 10 15
 Glu Leu Asp Val Leu Lys Gly Thr Leu Gly Gln Asp Val Ile Asp Ile
 20 25 30
 Arg Thr Leu Gly Ser Lys Gly Val Phe Thr Phe Asp Pro Gly Phe Thr
 35 40 45
 Ser Thr Ala Ser Cys Glu Ser Lys Ile Thr Phe Ile Asp Gly Asp Glu
 50 55 60
 Gly Ile Leu Leu His Arg Gly Phe Pro Ile Asp Gln Leu Ala Thr Asp
 65 70 75 80
 Ser Asn Tyr Leu Glu Val Cys Tyr Ile Leu Leu Asn Gly Glu Lys Pro

				85				90					95			
Thr	Gln	Glu	Gln	Tyr	Asp	Glu	Phe	Lys	Thr	Thr	Val	Thr	Arg	His	Thr	
			100					105					110			
Met	Ile	His	Glu	Gln	Ile	Thr	Arg	Leu	Phe	His	Ala	Phe	Arg	Arg	Asp	
		115					120					125				
Ser	His	Pro	Met	Ala	Val	Met	Cys	Gly	Ile	Thr	Gly	Ala	Leu	Ala	Ala	
		130				135					140					
Phe	Tyr	His	Asp	Ser	Leu	Asp	Val	Asn	Asn	Pro	Arg	His	Arg	Glu	Ile	
145					150					155					160	
Ala	Ala	Phe	Arg	Leu	Leu	Ser	Lys	Met	Pro	Thr	Met	Ala	Ala	Met	Cys	
			165					170						175		
Tyr	Lys	Tyr	Ser	Ile	Gly	Gln	Pro	Phe	Val	Tyr	Pro	Arg	Asn	Asp	Leu	
			180					185					190			
Ser	Tyr	Ala	Gly	Asn	Phe	Leu	Asn	Met	Met	Phe	Ser	Thr	Pro	Cys	Glu	
		195				200						205				
Pro	Tyr	Glu	Val	Asn	Pro	Ile	Leu	Glu	Arg	Ala	Met	Asp	Arg	Ile	Leu	
		210				215					220					
Ile	Leu	His	Ala	Asp	His	Glu	Gln	Asn	Ala	Ser	Thr	Ser	Thr	Val	Arg	
225					230					235					240	
Thr	Ala	Gly	Ser	Ser	Gly	Ala	Asn	Pro	Phe	Ala	Cys	Ile	Ala	Ala	Gly	
			245					250						255		
Ile	Ala	Ser	Leu	Trp	Gly	Pro	Ala	His	Gly	Gly	Ala	Asn	Glu	Ala	Ala	
			260					265					270			
Leu	Lys	Met	Leu	Glu	Glu	Ile	Ser	Ser	Val	Lys	His	Ile	Pro	Glu	Phe	
		275					280					285				
Val	Arg	Arg	Ala	Lys	Asp	Lys	Asn	Asp	Ser	Phe	Arg	Leu	Met	Gly	Phe	
		290				295					300					
Gly	His	Arg	Val	Tyr	Lys	Asn	Tyr	Asp	Pro	Arg	Ala	Thr	Val	Met	Arg	
305					310					315					320	
Glu	Thr	Cys	His	Glu	Val	Leu	Lys	Glu	Leu	Gly	Thr	Lys	Asp	Asp	Leu	
			325					330						335		
Leu	Glu	Val	Ala	Met	Glu	Leu	Glu	Asn	Ile	Ala	Leu	Asn	Asp	Pro	Tyr	
			340					345					350			
Phe	Ile	Glu	Lys	Lys	Leu	Tyr	Pro	Asn	Val	Asp	Phe	Tyr	Ser	Gly	Ile	
		355					360					365				
Ile	Leu	Lys	Ala	Met	Gly	Ile	Pro	Ser	Ser	Met	Phe	Thr	Val	Ile	Phe	
		370				375					380					
Ala	Met	Ala	Arg	Thr	Val	Gly	Trp	Ile	Ala	His	Trp	Ser	Glu	Met	His	
385					390					395					400	
Ser	Asp	Gly	Met	Lys	Ile	Ala	Arg	Pro	Arg	Gln	Leu	Tyr	Thr	Gly	Tyr	
			405					410						415		
Glu	Lys	Arg	Asp	Phe	Lys	Ser	Asp	Ile	Lys	Arg						
			420					425								

<210> 325
 <211> 477
 <212> PRT
 <213> E. Coli

				<400>												
Met	Lys	Val	Thr	Leu	Pro	Glu	Phe	Glu	Arg	Ala	Gly	Val	Met	Val	Val	
1				5				10					15			
Gly	Asp	Val	Met	Leu	Asp	Arg	Tyr	Trp	Tyr	Gly	Pro	Thr	Ser	Arg	Ile	
			20					25				30				
Ser	Pro	Glu	Ala	Pro	Val	Pro	Val	Val	Lys	Val	Asn	Thr	Ile	Glu	Glu	
		35					40					45				

Arg	Pro	Gly	Gly	Ala	Ala	Asn	Val	Ala	Met	Asn	Ile	Ala	Ser	Leu	Gly
50						55					60				
Ala	Asn	Ala	Arg	Leu	Val	Gly	Leu	Thr	Gly	Ile	Asp	Asp	Ala	Ala	Arg
65					70					75					80
Ala	Leu	Ser	Lys	Ser	Leu	Ala	Asp	Val	Asn	Val	Lys	Cys	Asp	Phe	Val
				85					90					95	
Ser	Val	Pro	Thr	His	Pro	Thr	Ile	Thr	Lys	Leu	Arg	Val	Leu	Ser	Arg
			100					105					110		
Asn	Gln	Gln	Leu	Ile	Arg	Leu	Asp	Phe	Glu	Glu	Gly	Phe	Glu	Gly	Val
		115					120					125			
Asp	Pro	Gln	Pro	Leu	His	Glu	Arg	Ile	Asn	Gln	Ala	Leu	Ser	Ser	Ile
	130					135					140				
Gly	Ala	Leu	Val	Leu	Ser	Asp	Tyr	Ala	Lys	Gly	Ala	Leu	Ala	Ser	Val
145					150					155					160
Gln	Gln	Met	Ile	Gln	Leu	Ala	Arg	Lys	Ala	Gly	Val	Pro	Val	Leu	Ile
				165					170					175	
Asp	Pro	Lys	Gly	Thr	Asp	Phe	Glu	Arg	Tyr	Arg	Gly	Ala	Thr	Leu	Leu
			180					185					190		
Thr	Pro	Asn	Leu	Ser	Glu	Phe	Glu	Ala	Val	Val	Gly	Lys	Cys	Lys	Thr
		195					200					205			
Glu	Glu	Glu	Ile	Val	Glu	Arg	Gly	Met	Lys	Leu	Ile	Ala	Asp	Tyr	Glu
		210				215					220				
Leu	Ser	Ala	Leu	Leu	Val	Thr	Arg	Ser	Glu	Gln	Gly	Met	Ser	Leu	Leu
225					230					235					240
Gln	Pro	Gly	Lys	Ala	Pro	Leu	His	Met	Pro	Thr	Gln	Ala	Gln	Glu	Val
				245					250					255	
Tyr	Asp	Val	Thr	Gly	Ala	Gly	Asp	Thr	Val	Ile	Gly	Val	Leu	Ala	Ala
			260				265						270		
Thr	Leu	Ala	Ala	Gly	Asn	Ser	Leu	Glu	Glu	Ala	Cys	Phe	Phe	Ala	Asn
		275					280					285			
Ala	Ala	Ala	Gly	Val	Val	Val	Gly	Lys	Leu	Gly	Thr	Ser	Thr	Val	Ser
		290				295					300				
Pro	Ile	Glu	Leu	Glu	Asn	Ala	Val	Arg	Gly	Arg	Ala	Asp	Thr	Gly	Phe
					310					315					320
Gly	Val	Met	Thr	Glu	Glu	Glu	Leu	Lys	Leu	Ala	Val	Ala	Ala	Ala	Arg
				325					330					335	
Lys	Arg	Gly	Glu	Lys	Val	Val	Met	Thr	Asn	Gly	Val	Phe	Asp	Ile	Leu
			340					345					350		
His	Ala	Gly	His	Val	Ser	Tyr	Leu	Ala	Asn	Ala	Arg	Lys	Leu	Gly	Asp
		355					360					365			
Arg	Leu	Ile	Val	Ala	Val	Asn	Ser	Asp	Ala	Ser	Thr	Lys	Arg	Leu	Lys
		370				375						380			
Gly	Asp	Ser	Arg	Pro	Val	Asn	Pro	Leu	Glu	Gln	Arg	Met	Ile	Val	Leu
385					390					395					400
Gly	Ala	Leu	Glu	Ala	Val	Asp	Trp	Val	Val	Ser	Phe	Glu	Glu	Asp	Thr
				405					410					415	
Pro	Gln	Arg	Leu	Ile	Ala	Gly	Ile	Leu	Pro	Asp	Leu	Leu	Val	Lys	Gly
			420					425					430		
Gly	Asp	Tyr	Lys	Pro	Glu	Glu	Ile	Ala	Gly	Ser	Lys	Glu	Val	Trp	Ala
		435					440					445			
Asn	Gly	Gly	Glu	Val	Leu	Val	Leu	Asn	Phe	Glu	Asp	Gly	Cys	Ser	Thr
	450					455					460				
Thr	Asn	Ile	Ile	Lys	Lys	Ile	Gln	Gln	Asp	Lys	Lys	Gly			
465					470					475					

<210> 326

<211> 946
 <212> PRT
 <213> E. Coli

<400> 326

Met	Lys	Pro	Leu	Ser	Ser	Pro	Leu	Gln	Gln	Tyr	Trp	Gln	Thr	Val	Val
1				5					10					15	
Glu	Arg	Leu	Pro	Glu	Pro	Leu	Ala	Glu	Glu	Ser	Leu	Ser	Ala	Gln	Ala
		20						25					30		
Lys	Ser	Val	Leu	Thr	Phe	Ser	Asp	Phe	Val	Gln	Asp	Ser	Val	Ile	Ala
		35					40					45			
His	Pro	Glu	Trp	Leu	Thr	Glu	Leu	Glu	Ser	Gln	Pro	Pro	Gln	Ala	Asp
	50					55					60				
Glu	Trp	Gln	His	Tyr	Ala	Ala	Trp	Leu	Gln	Glu	Ala	Leu	Cys	Asn	Val
65				70					75						80
Ser	Asp	Glu	Ala	Gly	Leu	Met	Arg	Glu	Leu	Arg	Leu	Phe	Arg	Arg	Arg
				85					90					95	
Ile	Met	Val	Arg	Ile	Ala	Trp	Ala	Gln	Thr	Leu	Ala	Leu	Val	Thr	Glu
			100					105					110		
Glu	Ser	Ile	Leu	Gln	Gln	Leu	Ser	Tyr	Leu	Ala	Glu	Thr	Leu	Ile	Val
		115					120					125			
Ala	Ala	Arg	Asp	Trp	Leu	Tyr	Asp	Ala	Cys	Cys	Arg	Glu	Trp	Gly	Thr
	130					135					140				
Pro	Cys	Asn	Ala	Gln	Gly	Glu	Ala	Gln	Pro	Leu	Leu	Ile	Leu	Gly	Met
145					150					155					160
Gly	Lys	Leu	Gly	Gly	Gly	Glu	Leu	Asn	Phe	Ser	Ser	Asp	Ile	Asp	Leu
			165						170					175	
Ile	Phe	Ala	Trp	Pro	Glu	His	Gly	Cys	Thr	Gln	Gly	Gly	Arg	Arg	Glu
		180					185						190		
Leu	Asp	Asn	Ala	Gln	Phe	Phe	Thr	Arg	Met	Gly	Gln	Arg	Leu	Ile	Lys
	195						200					205			
Val	Leu	Asp	Gln	Pro	Thr	Gln	Asp	Gly	Phe	Val	Tyr	Arg	Val	Asp	Met
	210					215					220				
Arg	Leu	Arg	Pro	Phe	Gly	Glu	Ser	Gly	Pro	Leu	Val	Leu	Ser	Phe	Ala
225					230					235					240
Ala	Leu	Glu	Asp	Tyr	Tyr	Gln	Glu	Gln	Gly	Arg	Asp	Trp	Glu	Arg	Tyr
			245						250					255	
Ala	Met	Val	Lys	Ala	Arg	Ile	Met	Gly	Asp	Ser	Glu	Gly	Val	Tyr	Ala
		260						265					270		
Asn	Glu	Leu	Arg	Ala	Met	Leu	Arg	Pro	Phe	Val	Phe	Arg	Arg	Tyr	Ile
	275						280					285			
Asp	Phe	Ser	Val	Ile	Gln	Ser	Leu	Arg	Asn	Met	Lys	Gly	Met	Ile	Ala
	290					295					300				
Arg	Glu	Val	Arg	Arg	Arg	Gly	Leu	Thr	Asp	Asn	Ile	Lys	Leu	Gly	Ala
305					310					315					320
Gly	Gly	Ile	Arg	Glu	Ile	Glu	Phe	Ile	Val	Gln	Val	Phe	Gln	Leu	Ile
			325						330					335	
Arg	Gly	Gly	Arg	Glu	Pro	Ser	Leu	Gln	Ser	Arg	Ser	Leu	Leu	Pro	Thr
		340						345					350		
Leu	Ser	Ala	Ile	Ala	Glu	Leu	His	Leu	Leu	Ser	Glu	Asn	Asp	Ala	Glu
		355					360					365			
Gln	Leu	Arg	Val	Ala	Tyr	Leu	Phe	Leu	Arg	Arg	Leu	Glu	Asn	Leu	Leu
	370					375					380				
Gln	Ser	Ile	Asn	Asp	Glu	Gln	Thr	Gln	Thr	Leu	Pro	Ser	Asp	Glu	Leu
385					390					395					400
Asn	Arg	Ala	Arg	Leu	Ala	Trp	Ala	Met	Asp	Phe	Ala	Asp	Trp	Pro	Gln
				405					410					415	

Leu	Thr	Gly	Ala	Leu	Thr	Ala	His	Met	Thr	Asn	Val	Arg	Arg	Val	Phe
			420					425						430	
Asn	Glu	Leu	Ile	Gly	Asp	Asp	Glu	Ser	Glu	Thr	Gln	Glu	Glu	Ser	Leu
		435					440					445			
Ser	Glu	Gln	Trp	Arg	Glu	Leu	Trp	Gln	Asp	Ala	Leu	Gln	Glu	Asp	Asp
	450					455					460				
Thr	Thr	Pro	Val	Leu	Ala	His	Leu	Ser	Glu	Asp	Asp	Arg	Lys	Gln	Val
465					470					475					480
Leu	Thr	Leu	Ile	Ala	Asp	Phe	Arg	Lys	Glu	Leu	Asp	Lys	Arg	Thr	Ile
				485					490					495	
Gly	Pro	Arg	Gly	Arg	Gln	Val	Leu	Asp	His	Leu	Met	Pro	His	Leu	Leu
			500					505					510		
Ser	Asp	Val	Cys	Ala	Arg	Glu	Asp	Ala	Ala	Val	Thr	Leu	Ser	Arg	Ile
		515					520					525			
Thr	Ala	Leu	Leu	Val	Gly	Ile	Val	Thr	Arg	Thr	Thr	Tyr	Leu	Glu	Leu
	530					535					540				
Leu	Ser	Glu	Phe	Pro	Ala	Ala	Leu	Lys	His	Leu	Ile	Ser	Leu	Cys	Ala
545					550					555					560
Ala	Ser	Pro	Met	Ile	Ala	Ser	Gln	Leu	Ala	Arg	Tyr	Pro	Leu	Leu	Leu
				565					570					575	
Asp	Glu	Leu	Leu	Asp	Pro	Asn	Thr	Leu	Tyr	Gln	Pro	Thr	Ala	Thr	Asp
			580					585					590		
Ala	Tyr	Arg	Asp	Glu	Leu	Arg	Gln	Tyr	Leu	Leu	Arg	Val	Pro	Glu	Asp
		595					600					605			
Asp	Glu	Glu	Gln	Gln	Leu	Glu	Ala	Leu	Arg	Gln	Phe	Lys	Gln	Ala	Gln
	610					615					620				
Leu	Leu	Arg	Ile	Ala	Ala	Ala	Asp	Ile	Ala	Gly	Thr	Leu	Pro	Val	Met
625					630					635					640
Lys	Val	Ser	Asp	His	Leu	Thr	Trp	Leu	Ala	Glu	Ala	Met	Ile	Asp	Ala
				645					650				655		
Val	Val	Gln	Gln	Ala	Trp	Val	Gln	Met	Val	Ala	Arg	Tyr	Gly	Lys	Pro
			660					665					670		
Asn	His	Leu	Asn	Glu	Arg	Glu	Gly	Arg	Gly	Phe	Ala	Val	Val	Gly	Tyr
		675					680					685			
Gly	Lys	Leu	Gly	Gly	Trp	Glu	Leu	Gly	Tyr	Ser	Ser	Asp	Leu	Asp	Leu
	690					695					700				
Ile	Phe	Leu	His	Asp	Cys	Pro	Met	Asp	Ala	Met	Thr	Asp	Gly	Glu	Arg
705					710					715					720
Glu	Ile	Asp	Gly	Arg	Gln	Phe	Tyr	Leu	Arg	Leu	Ala	Gln	Arg	Ile	Met
				725					730					735	
His	Leu	Phe	Ser	Thr	Arg	Thr	Ser	Ser	Gly	Ile	Leu	Tyr	Glu	Val	Asp
			740					745					750		
Ala	Arg	Leu	Arg	Pro	Ser	Gly	Ala	Ala	Gly	Met	Leu	Val	Thr	Ser	Ala
		755					760					765			
Glu	Ala	Phe	Ala	Asp	Tyr	Gln	Lys	Asn	Glu	Ala	Trp	Thr	Trp	Glu	His
	770					775					780				
Gln	Ala	Leu	Val	Arg	Ala	Arg	Val	Val	Tyr	Gly	Asp	Pro	Gln	Leu	Thr
785					790					795					800
Ala	His	Phe	Asp	Ala	Val	Arg	Arg	Glu	Ile	Met	Thr	Leu	Pro	Arg	Glu
				805					810					815	
Gly	Lys	Thr	Leu	Gln	Thr	Glu	Val	Arg	Glu	Met	Arg	Glu	Lys	Met	Arg
			820					825					830		
Ala	His	Leu	Gly	Asn	Lys	His	Arg	Asp	Arg	Phe	Asp	Ile	Lys	Ala	Asp
		835					840					845			
Glu	Gly	Gly	Ile	Thr	Asp	Ile	Glu	Phe	Ile	Thr	Gln	Tyr	Leu	Val	Leu
	850					855					860				
Arg	Tyr	Ala	His	Glu	Lys	Pro	Lys	Leu	Thr	Arg	Trp	Ser	Asp	Asn	Val

865					870					875					880
Arg	Ile	Leu	Glu	Leu	Leu	Ala	Gln	Asn	Asp	Ile	Met	Glu	Glu	Gln	Glu
				885					890					895	
Ala	Met	Ala	Leu	Thr	Arg	Ala	Tyr	Thr	Thr	Leu	Arg	Asp	Glu	Leu	His
			900					905					910		
His	Leu	Ala	Leu	Gln	Glu	Leu	Pro	Gly	His	Val	Ser	Glu	Asp	Cys	Phe
		915					920					925			
Thr	Ala	Glu	Arg	Glu	Leu	Val	Arg	Ala	Ser	Trp	Gln	Lys	Trp	Leu	Val
	930					935					940				
Glu	Glu														
945															

<210> 327
 <211> 433
 <212> PRT
 <213> E. Coli

<400> 327

Met	Ala	Gln	Glu	Ile	Glu	Leu	Lys	Phe	Ile	Val	Asn	His	Ser	Ala	Val
1				5					10					15	
Glu	Ala	Leu	Arg	Asp	His	Leu	Asn	Thr	Leu	Gly	Gly	Glu	His	His	Asp
			20					25					30		
Pro	Val	Gln	Leu	Leu	Asn	Ile	Tyr	Tyr	Glu	Thr	Pro	Asp	Asn	Trp	Leu
		35				40						45			
Arg	Gly	His	Asp	Met	Gly	Leu	Arg	Ile	Arg	Gly	Glu	Asn	Gly	Arg	Tyr
	50				55						60				
Glu	Met	Thr	Met	Lys	Val	Ala	Gly	Arg	Val	Thr	Gly	Gly	Leu	His	Gln
65				70					75					80	
Arg	Pro	Glu	Tyr	Asn	Val	Ala	Leu	Ser	Glu	Pro	Thr	Leu	Asp	Leu	Ala
			85					90						95	
Gln	Leu	Pro	Thr	Glu	Val	Trp	Pro	Asn	Gly	Glu	Leu	Pro	Ala	Asp	Leu
		100					105						110		
Ala	Ser	Arg	Val	Gln	Pro	Leu	Phe	Ser	Thr	Asp	Phe	Tyr	Arg	Glu	Lys
		115					120					125			
Trp	Leu	Val	Ala	Val	Asp	Gly	Ser	Gln	Ile	Glu	Ile	Ala	Leu	Asp	Gln
	130					135					140				
Gly	Glu	Val	Lys	Ala	Gly	Glu	Phe	Ala	Glu	Pro	Ile	Cys	Glu	Leu	Glu
145				150					155					160	
Leu	Glu	Leu	Leu	Ser	Gly	Asp	Thr	Arg	Ala	Val	Leu	Lys	Leu	Ala	Asn
			165					170						175	
Gln	Leu	Val	Ser	Gln	Thr	Gly	Leu	Arg	Gln	Gly	Ser	Leu	Ser	Lys	Ala
		180					185						190		
Ala	Arg	Gly	Tyr	His	Leu	Ala	Gln	Gly	Asn	Pro	Ala	Arg	Glu	Ile	Lys
	195					200						205			
Pro	Thr	Thr	Ile	Leu	His	Val	Ala	Ala	Lys	Ala	Asp	Val	Glu	Gln	Gly
	210				215						220				
Leu	Glu	Ala	Ala	Leu	Glu	Leu	Ala	Leu	Ala	Gln	Trp	Gln	Tyr	His	Glu
225				230					235					240	
Glu	Leu	Trp	Val	Arg	Gly	Asn	Asp	Ala	Ala	Lys	Glu	Gln	Val	Leu	Ala
			245					250						255	
Ala	Ile	Ser	Leu	Val	Arg	His	Thr	Leu	Met	Leu	Phe	Gly	Gly	Ile	Val
		260					265					270			
Pro	Arg	Lys	Ala	Ser	Thr	His	Leu	Arg	Asp	Leu	Leu	Thr	Gln	Cys	Glu
	275					280						285			
Ala	Thr	Ile	Ala	Ser	Ala	Val	Ser	Ala	Val	Thr	Ala	Val	Tyr	Ser	Thr

290		295		300
Glu Thr Ala Met Ala Lys Leu Ala Leu Thr Glu Trp Leu Val Ser Lys				
305		310		315
Ala Trp Gln Pro Phe Leu Asp Ala Lys Ala Gln Gly Lys Ile Ser Asp				
	325		330	335
Ser Phe Lys Arg Phe Ala Asp Ile His Leu Ser Arg His Ala Ala Glu				
	340		345	350
Leu Lys Ser Val Phe Cys Gln Pro Leu Gly Asp Arg Tyr Arg Asp Gln				
	355		360	365
Leu Pro Arg Leu Thr Arg Asp Ile Asp Ser Ile Leu Leu Leu Ala Gly				
	370		375	380
Tyr Tyr Asp Pro Val Val Ala Gln Ala Trp Leu Glu Asn Trp Gln Gly				
385		390		395
Leu His His Ala Ile Ala Thr Gly Gln Arg Ile Glu Ile Glu His Phe				
	405		410	415
Arg Asn Glu Ala Asn Asn Gln Glu Pro Phe Trp Leu His Ser Gly Lys				
	420		425	430
Arg				

<210> 328
 <211> 70
 <212> PRT
 <213> E. Coli

<400> 328
Met Ser Gly Lys Met Thr Gly Ile Val Lys Trp Phe Asn Ala Asp Lys
1 5 10 15
Gly Phe Gly Phe Ile Thr Pro Asp Asp Gly Ser Lys Asp Val Phe Val
20 25 30
His Phe Ser Ala Ile Gln Asn Asp Gly Tyr Lys Ser Leu Asp Glu Gly
35 40 45
Gln Lys Val Ser Phe Thr Ile Glu Ser Gly Ala Lys Gly Pro Ala Ala
50 55 60
Gly Asn Val Thr Ser Leu
65 70

<210> 329
 <211> 523
 <212> PRT
 <213> E. Coli

<400> 329
Met Arg Asp Ile Val Asp Pro Val Phe Ser Ile Gly Ile Ser Ser Leu
1 5 10 15
Trp Asp Glu Leu Arg His Met Pro Ala Gly Gly Val Trp Trp Phe Asn
20 25 30
Val Asp Arg His Glu Asp Ala Ile Ser Leu Ala Asn Gln Thr Ile Ala
35 40 45
Ser Gln Ala Glu Thr Ala His Val Ala Val Ile Ser Met Asp Ser Asp
50 55 60
Pro Ala Lys Ile Phe Gln Leu Asp Asp Ser Gln Gly Pro Glu Lys Ile
65 70 75 80

Lys	Leu	Phe	Ser	Met	Leu	Asn	His	Glu	Lys	Gly	Leu	Tyr	Tyr	Leu	Thr	
				85					90					95		
Arg	Asp	Leu	Gln	Cys	Ser	Ile	Asp	Pro	His	Asn	Tyr	Leu	Phe	Ile	Leu	
			100					105					110			
Val	Cys	Ala	Asn	Asn	Ala	Trp	Gln	Asn	Ile	Pro	Ala	Glu	Arg	Leu	Arg	
		115					120					125				
Ser	Trp	Leu	Asp	Lys	Met	Asn	Lys	Trp	Ser	Arg	Leu	Asn	His	Cys	Ser	
	130					135					140					
Leu	Leu	Val	Ile	Asn	Pro	Gly	Asn	Asn	Asn	Asp	Lys	Gln	Phe	Ser	Leu	
145				150						155					160	
Leu	Leu	Glu	Glu	Tyr	Arg	Ser	Leu	Phe	Gly	Leu	Ala	Ser	Leu	Arg	Phe	
			165						170					175		
Gln	Gly	Asp	Gln	His	Leu	Leu	Asp	Ile	Ala	Phe	Trp	Cys	Asn	Glu	Lys	
			180					185					190			
Gly	Val	Ser	Ala	Arg	Gln	Gln	Leu	Ser	Val	Gln	Gln	Gln	Asn	Gly	Ile	
	195						200					205				
Trp	Thr	Leu	Val	Gln	Ser	Glu	Glu	Ala	Glu	Ile	Gln	Pro	Arg	Ser	Asp	
	210					215					220					
Glu	Lys	Arg	Ile	Leu	Ser	Asn	Val	Ala	Val	Leu	Glu	Gly	Ala	Pro	Pro	
225				230						235					240	
Leu	Ser	Glu	His	Trp	Gln	Leu	Phe	Asn	Asn	Asn	Glu	Val	Leu	Phe	Asn	
			245					250						255		
Glu	Ala	Arg	Thr	Ala	Gln	Ala	Ala	Thr	Val	Val	Phe	Ser	Leu	Gln	Gln	
			260					265					270			
Asn	Ala	Gln	Ile	Glu	Pro	Leu	Ala	Arg	Ser	Ile	His	Thr	Leu	Arg	Arg	
	275						280					285				
Gln	Arg	Gly	Ser	Ala	Met	Lys	Ile	Leu	Val	Arg	Glu	Asn	Thr	Ala	Ser	
	290					295					300					
Leu	Arg	Ala	Thr	Asp	Glu	Arg	Leu	Leu	Leu	Ala	Cys	Gly	Ala	Asn	Met	
305				310						315					320	
Val	Ile	Pro	Trp	Asn	Ala	Pro	Leu	Ser	Arg	Cys	Leu	Thr	Met	Ile	Glu	
			325						330					335		
Ser	Val	Gln	Gly	Gln	Lys	Phe	Ser	Arg	Tyr	Val	Pro	Glu	Asp	Ile	Thr	
		340						345					350			
Thr	Leu	Leu	Ser	Met	Thr	Gln	Pro	Leu	Lys	Leu	Arg	Gly	Phe	Gln	Lys	
	355					360						365				
Trp	Asp	Val	Phe	Cys	Asn	Ala	Val	Asn	Asn	Met	Met	Asn	Asn	Pro	Leu	
	370					375					380					
Leu	Pro	Ala	His	Gly	Lys	Gly	Val	Leu	Val	Ala	Leu	Arg	Pro	Val	Pro	
385				390						395					400	
Gly	Ile	Arg	Val	Glu	Gln	Ala	Leu	Thr	Leu	Cys	Arg	Pro	Asn	Arg	Thr	
			405					410						415		
Gly	Asp	Ile	Met	Thr	Ile	Gly	Gly	Asn	Arg	Leu	Val	Leu	Phe	Leu	Ser	
			420					425					430			
Phe	Cys	Arg	Ile	Asn	Asp	Leu	Asp	Thr	Ala	Leu	Asn	His	Ile	Phe	Pro	
	435						440					445				
Leu	Pro	Thr	Gly	Asp	Ile	Phe	Ser	Asn	Arg	Met	Val	Trp	Phe	Glu	Asp	
	450					455					460					
Asp	Gln	Ile	Ser	Ala	Glu	Leu	Val	Gln	Met	Arg	Leu	Leu	Ala	Pro	Glu	
465				470						475					480	
Gln	Trp	Gly	Met	Pro	Leu	Pro	Leu	Thr	Gln	Ser	Ser	Lys	Pro	Val	Ile	
			485					490						495		
Asn	Ala	Glu	His	Asp	Gly	Arg	His	Trp	Arg	Arg	Ile	Pro	Glu	Pro	Met	
		500						505					510			
Arg	Leu	Leu	Asp	Asp	Ala	Val	Glu	Arg	Ser	Ser						
	515						520									

<210> 330
 <211> 62
 <212> PRT
 <213> E. Coli

<400> 330
 Met Thr Ile Ser Asp Ile Ile Glu Ile Ile Val Val Cys Ala Leu Ile
 1 5 10 15
 Phe Phe Pro Leu Gly Tyr Leu Ala Arg His Ser Leu Arg Arg Ile Arg
 20 25 30
 Asp Thr Leu Arg Leu Phe Phe Ala Lys Pro Arg Tyr Val Lys Pro Ala
 35 40 45
 Gly Thr Leu Arg Arg Thr Glu Lys Ala Arg Ala Thr Lys Lys
 50 55 60

<210> 331
 <211> 559
 <212> PRT
 <213> E. Coli

<400> 331
 Met Thr Gln Phe Thr Gln Asn Thr Ala Met Pro Ser Ser Leu Trp Gln
 1 5 10 15
 Tyr Trp Arg Gly Leu Ser Gly Trp Asn Phe Tyr Phe Leu Val Lys Phe
 20 25 30
 Gly Leu Leu Trp Ala Gly Tyr Leu Asn Phe His Pro Leu Leu Asn Leu
 35 40 45
 Val Phe Ala Ala Phe Leu Leu Met Pro Leu Pro Arg Tyr Ser Leu His
 50 55 60
 Arg Leu Arg His Trp Ile Ala Leu Pro Ile Gly Phe Ala Leu Phe Trp
 65 70 75 80
 His Asp Thr Trp Leu Pro Gly Pro Glu Ser Ile Met Ser Gln Gly Ser
 85 90 95
 Gln Val Ala Gly Phe Ser Thr Asp Tyr Leu Ile Asp Leu Val Thr Arg
 100 105 110
 Phe Ile Asn Trp Gln Met Ile Gly Ala Ile Phe Val Leu Leu Val Ala
 115 120 125
 Trp Leu Phe Leu Ser Gln Trp Ile Arg Ile Thr Val Phe Val Val Ala
 130 135 140
 Ile Leu Leu Trp Leu Asn Val Leu Thr Leu Ala Gly Pro Ser Phe Ser
 145 150 155 160
 Leu Trp Pro Ala Gly Gln Pro Thr Thr Thr Val Thr Thr Thr Gly Gly
 165 170 175
 Asn Ala Ala Ala Thr Val Ala Ala Thr Gly Gly Ala Pro Val Val Gly
 180 185 190
 Asp Met Pro Ala Gln Thr Ala Pro Pro Thr Thr Ala Asn Leu Asn Ala
 195 200 205
 Trp Leu Asn Asn Phe Tyr Asn Ala Glu Ala Lys Arg Lys Ser Thr Phe
 210 215 220
 Pro Ser Ser Leu Pro Ala Asp Ala Gln Pro Phe Glu Leu Leu Val Ile
 225 230 235 240
 Asn Ile Cys Ser Leu Ser Trp Ser Asp Ile Glu Ala Ala Gly Leu Met
 245 250 255
 Ser His Pro Leu Trp Ser His Phe Asp Ile Glu Phe Lys Asn Phe Asn
 260 265 270

Ser Ala Thr Ser Tyr Ser Gly Pro Ala Ala Ile Arg Leu Leu Arg Ala
275 280 285
Ser Cys Gly Gln Thr Ser His Thr Asn Leu Tyr Gln Pro Ala Asn Asn
290 295 300
Asp Cys Tyr Leu Phe Asp Asn Leu Ser Lys Leu Gly Phe Thr Gln His
305 310 315 320
Leu Met Met Gly His Asn Gly Gln Phe Gly Gly Phe Leu Lys Glu Val
325 330 335
Arg Glu Asn Gly Gly Met Gln Ser Glu Leu Met Asp Gln Thr Asn Leu
340 345 350
Pro Val Ile Leu Leu Gly Phe Asp Gly Ser Pro Val Tyr Asp Asp Thr
355 360 365
Ala Val Leu Asn Arg Trp Leu Asp Val Thr Glu Lys Asp Lys Asn Ser
370 375 380
Arg Ser Ala Thr Phe Tyr Asn Thr Leu Pro Leu His Asp Gly Asn His
385 390 395 400
Tyr Pro Gly Val Ser Lys Thr Ala Asp Tyr Lys Ala Arg Ala Gln Lys
405 410 415
Phe Phe Asp Glu Leu Asp Ala Phe Phe Thr Glu Leu Glu Lys Ser Gly
420 425 430
Arg Lys Val Met Val Val Val Val Pro Glu His Gly Gly Ala Leu Lys
435 440 445
Gly Asp Arg Met Gln Val Ser Gly Leu Arg Asp Ile Pro Ser Pro Ser
450 455 460
Ile Thr Asp Val Pro Val Gly Val Lys Phe Phe Gly Met Lys Ala Pro
465 470 475 480
His Gln Gly Ala Pro Ile Val Ile Glu Gln Pro Ser Ser Phe Leu Ala
485 490 495
Ile Ser Asp Leu Val Val Arg Val Leu Asp Gly Lys Ile Phe Thr Glu
500 505 510
Asp Asn Val Asp Trp Lys Lys Leu Thr Ser Gly Leu Pro Gln Thr Ala
515 520 525
Pro Val Ser Glu Asn Ser Asn Ala Val Val Ile Gln Tyr Gln Asp Lys
530 535 540
Pro Tyr Val Arg Leu Asn Gly Gly Asp Trp Val Pro Tyr Pro Gln
545 550 555

<210> 332
<211> 127
<212> PRT
<213> E. Coli

<400> 332
Met Glu Gly Ser Arg Met Lys Tyr Arg Ile Ala Leu Ala Val Ser Leu
1 5 10 15
Phe Ala Leu Ser Ala Gly Ser Tyr Ala Thr Thr Leu Cys Gln Glu Lys
20 25 30
Glu Gln Asn Ile Leu Lys Glu Ile Ser Tyr Ala Glu Lys His Gln Asn
35 40 45
Gln Asn Arg Ile Asp Gly Leu Asn Lys Ala Leu Ser Glu Val Arg Ala
50 55 60
Asn Cys Ser Asp Ser Gln Leu Arg Ala Asp His Gln Lys Lys Ile Ala
65 70 75 80
Lys Gln Lys Asp Glu Val Ala Glu Arg Gln Gln Asp Leu Ala Glu Ala
85 90 95
Lys Gln Lys Gly Asp Ala Asp Lys Ile Ala Lys Arg Glu Arg Lys Leu

[illegible][illegible][illegible][illegible][illegible][illegible]

<213> E. Coli

<400> 335

Met Ser Ser Lys Val Glu Arg Glu Arg Arg Lys Ala Gln Leu Leu Ser
1 5 10 15
Gln Ile Gln Gln Gln Arg Leu Asp Leu Ser Ala Ser Arg Arg Glu Trp
20 25 30
Leu Glu Thr Thr Gly Ala Tyr Asp Arg Arg Trp Asn Met Leu Leu Ser
35 40 45
Leu Arg Ser Trp Ala Leu Val Gly Ser Ser Val Met Ala Ile Trp Thr
50 55 60
Ile Arg His Pro Asn Met Leu Val Arg Trp Ala Arg Arg Gly Phe Gly
65 70 75 80
Val Trp Ser Ala Trp Arg Leu Val Lys Thr Thr Leu Lys Gln Gln Gln
85 90 95
Leu Arg Gly

<210> 336

<211> 160

<212> PRT

<213> E. Coli

<400> 336

Met Ile Leu Ser Ile Asp Ser Asn Asp Ala Asn Thr Ala Pro Leu His
1 5 10 15
Lys Lys Thr Ile Ser Ser Leu Ser Gly Ala Val Glu Ser Met Met Lys
20 25 30
Lys Leu Glu Asp Val Gly Val Leu Val Ala Arg Ile Leu Met Pro Ile
35 40 45
Leu Phe Ile Thr Ala Gly Trp Gly Lys Ile Thr Gly Tyr Ala Gly Thr
50 55 60
Gln Gln Tyr Met Glu Ala Met Gly Val Pro Gly Phe Met Leu Pro Leu
65 70 75 80
Val Ile Leu Leu Glu Phe Gly Gly Gly Leu Ala Ile Leu Phe Gly Phe
85 90 95
Leu Thr Arg Thr Thr Ala Leu Phe Thr Ala Gly Phe Thr Leu Leu Thr
100 105 110
Ala Phe Leu Phe His Ser Asn Phe Ala Glu Gly Val Asn Ser Leu Met
115 120 125
Phe Met Lys Asn Leu Thr Ile Ser Gly Gly Phe Leu Leu Leu Ala Ile
130 135 140
Thr Gly Pro Gly Ala Tyr Ser Ile Asp Arg Leu Leu Asn Lys Lys Trp
145 150 155 160

<210> 337

<211> 296

<212> PRT

<213> E. Coli

<400> 337

Met Ile Lys Lys Thr Thr Glu Ile Asp Ala Ile Leu Leu Asn Leu Asn
1 5 10 15

Lys	Ala	Ile	Asp	Ala	His	Tyr	Gln	Trp	Leu	Val	Ser	Met	Phe	His	Ser
			20					25					30		
Val	Val	Ala	Arg	Asp	Ala	Ser	Lys	Pro	Glu	Ile	Thr	Asp	Asn	His	Ser
		35					40					45			
Tyr	Gly	Leu	Cys	Gln	Phe	Gly	Arg	Trp	Ile	Asp	His	Leu	Gly	Pro	Leu
	50					55				60					
Asp	Asn	Asp	Glu	Leu	Pro	Tyr	Val	Arg	Leu	Met	Asp	Ser	Ala	His	Gln
65					70					75					80
His	Met	His	Asn	Cys	Gly	Arg	Glu	Leu	Met	Leu	Ala	Ile	Val	Glu	Asn
			85						90					95	
His	Trp	Gln	Asp	Ala	His	Phe	Asp	Ala	Phe	Gln	Glu	Gly	Leu	Leu	Ser
			100					105					110		
Phe	Thr	Ala	Ala	Leu	Thr	Asp	Tyr	Lys	Ile	Tyr	Leu	Leu	Thr	Ile	Arg
		115					120					125			
Ser	Asn	Met	Asp	Val	Leu	Thr	Gly	Leu	Pro	Gly	Arg	Arg	Val	Leu	Asp
	130					135					140				
Glu	Ser	Phe	Asp	His	Gln	Leu	Arg	Asn	Ala	Glu	Pro	Leu	Asn	Leu	Tyr
145					150					155					160
Leu	Met	Leu	Leu	Asp	Ile	Asp	Arg	Phe	Lys	Leu	Val	Asn	Asp	Thr	Tyr
				165					170					175	
Gly	His	Leu	Ile	Gly	Asp	Val	Val	Leu	Arg	Thr	Leu	Ala	Thr	Tyr	Leu
			180					185					190		
Ala	Ser	Trp	Thr	Arg	Asp	Tyr	Glu	Thr	Val	Tyr	Arg	Tyr	Gly	Gly	Glu
		195					200					205			
Glu	Phe	Ile	Ile	Ile	Val	Lys	Ala	Ala	Asn	Asp	Glu	Glu	Ala	Cys	Arg
	210					215					220				
Ala	Gly	Val	Arg	Ile	Cys	Gln	Leu	Val	Asp	Asn	His	Ala	Ile	Thr	His
225					230					235					240
Ser	Glu	Gly	His	Ile	Asn	Ile	Thr	Val	Thr	Ala	Gly	Val	Ser	Arg	Ala
				245					250					255	
Phe	Pro	Glu	Glu	Pro	Leu	Asp	Val	Val	Ile	Gly	Arg	Ala	Asp	Arg	Ala
			260					265					270		
Met	Tyr	Glu	Gly	Lys	Gln	Thr	Gly	Arg	Asn	Arg	Cys	Met	Phe	Ile	Asp
		275					280					285			
Glu	Gln	Asn	Val	Ile	Asn	Arg	Val								
	290					295									

<210> 338
 <211> 203
 <212> PRT
 <213> E. Coli

<400> 338															
Met	Arg	Leu	Arg	Val	Val	Pro	Gly	Phe	Ile	Ser	Pro	Pro	Pro	Gly	Phe
1				5					10					15	
Gly	Gly	Leu	Gly	Tyr	Thr	Pro	Thr	Ala	Arg	Ala	Cys	Val	Asn	Ile	Ser
			20					25					30		
Ile	Pro	Leu	Gln	Leu	Arg	Val	Ile	Asp	Met	Leu	Asp	Val	Phe	Thr	Pro
		35					40					45			
Leu	Leu	Lys	Leu	Phe	Ala	Asn	Glu	Pro	Leu	Glu	Arg	Leu	Met	Tyr	Thr
	50					55					60				
Ile	Ile	Ile	Phe	Gly	Leu	Thr	Leu	Trp	Leu	Ile	Pro	Lys	Glu	Phe	Thr
65					70					75					80
Val	Ala	Phe	Asn	Ala	Tyr	Thr	Glu	Ile	Pro	Trp	Leu	Phe	Gln	Ile	Ile
				85					90					95	

Val	Phe	Ala	Phe	Ser	Phe	Val	Val	Ala	Ile	Ser	Phe	Ser	Arg	Leu	Arg
			100					105					110		
Ala	His	Ile	Gln	Lys	His	Tyr	Ser	Leu	Leu	Pro	Glu	Gln	Arg	Val	Leu
			115					120					125		
Leu	Arg	Leu	Ser	Glu	Lys	Glu	Ile	Ala	Val	Phe	Lys	Asp	Phe	Leu	Lys
			130					135				140			
Thr	Gly	Asn	Leu	Ile	Ile	Thr	Ser	Pro	Cys	Arg	Asn	Pro	Val	Met	Lys
								150				155			160
Lys	Leu	Glu	Arg	Lys	Gly	Ile	Ile	Gln	His	Gln	Ser	Asp	Ser	Ala	Asn
				165				170						175	
Cys	Ser	Tyr	Tyr	Leu	Val	Thr	Glu	Lys	Tyr	Ser	His	Phe	Met	Lys	Leu
			180					185					190		
Phe	Trp	Asn	Ser	Arg	Ser	Arg	Arg	Phe	Asn	Arg					
			195				200								

<210> 339
 <211> 58
 <212> PRT
 <213> E. Coli

<400> 339

Met	Leu	Leu	Gln	Pro	Ser	Ala	Arg	Thr	Ser	Phe	Gly	Phe	Lys	Cys	Phe
1				5					10					15	
Ala	Phe	Gly	Ile	Arg	His	Gly	Ser	Glu	Arg	Ser	Ile	Leu	Val	Gly	Glu
			20					25					30		
His	Ala	Ala	His	Gln	Gly	Phe	Val	Val	Ala	Glu	Val	Asp	Phe	Leu	His
			35				40					45			
Phe	Ala	Asn	Leu	Thr	Ser	Cys	Cys	Tyr	Val						
			50			55									

<210> 340
 <211> 1426
 <212> PRT
 <213> E. Coli

<400> 340

Met	Ser	Gly	Lys	Pro	Ala	Ala	Arg	Gln	Gly	Asp	Met	Thr	Gln	Tyr	Gly
1				5					10					15	
Gly	Pro	Ile	Val	Gln	Gly	Ser	Ala	Gly	Val	Arg	Ile	Gly	Ala	Pro	Thr
			20					25					30		
Gly	Val	Ala	Cys	Ser	Val	Cys	Pro	Gly	Gly	Met	Thr	Ser	Gly	Asn	Pro
			35				40					45			
Val	Asn	Pro	Leu	Leu	Gly	Ala	Lys	Val	Leu	Pro	Gly	Glu	Thr	Asp	Leu
	50				55						60				
Ala	Leu	Pro	Gly	Pro	Leu	Pro	Phe	Ile	Leu	Ser	Arg	Thr	Tyr	Ser	Ser
65				70					75					80	
Tyr	Arg	Thr	Lys	Thr	Pro	Ala	Pro	Val	Gly	Val	Phe	Gly	Pro	Gly	Trp
			85					90					95		
Lys	Ala	Pro	Ser	Asp	Ile	Arg	Leu	Gln	Leu	Arg	Asp	Asp	Gly	Leu	Ile
			100					105					110		
Leu	Asn	Asp	Asn	Gly	Gly	Arg	Ser	Ile	His	Phe	Glu	Pro	Leu	Leu	Pro
			115				120					125			
Gly	Glu	Ala	Val	Tyr	Ser	Arg	Ser	Glu	Ser	Met	Trp	Leu	Val	Arg	Gly
			130			135					140				

Gly	Lys	Ala	Ala	Gln	Pro	Asp	Gly	His	Thr	Leu	Ala	Arg	Leu	Trp	Gly
145					150					155					160
Ala	Leu	Pro	Pro	Asp	Ile	Arg	Leu	Ser	Pro	His	Leu	Tyr	Leu	Ala	Thr
				165					170						175
Asn	Ser	Ala	Gln	Gly	Pro	Trp	Trp	Ile	Leu	Gly	Trp	Ser	Glu	Arg	Val
			180					185					190		
Pro	Gly	Ala	Glu	Asp	Val	Leu	Pro	Ala	Pro	Leu	Pro	Pro	Tyr	Arg	Val
		195					200					205			
Leu	Thr	Gly	Met	Ala	Asp	Arg	Phe	Gly	Arg	Thr	Leu	Thr	Tyr	Arg	Arg
	210					215					220				
Glu	Ala	Ala	Gly	Asp	Leu	Ala	Gly	Glu	Ile	Thr	Gly	Val	Thr	Asp	Gly
225					230					235					240
Ala	Gly	Arg	Glu	Phe	Arg	Leu	Val	Leu	Thr	Thr	Gln	Ala	Gln	Arg	Ala
				245					250						255
Glu	Glu	Ala	Arg	Thr	Ser	Ser	Leu	Ser	Ser	Ser	Asp	Ser	Ser	Arg	Pro
			260					265					270		
Leu	Ser	Ala	Ser	Ala	Phe	Pro	Asp	Thr	Leu	Pro	Gly	Thr	Glu	Tyr	Gly
		275					280					285			
Pro	Asp	Arg	Gly	Ile	Arg	Leu	Ser	Ala	Val	Trp	Leu	Met	His	Asp	Pro
	290					295					300				
Ala	Tyr	Pro	Glu	Ser	Leu	Pro	Ala	Ala	Pro	Leu	Val	Arg	Tyr	Thr	Tyr
305					310					315					320
Thr	Glu	Ala	Gly	Glu	Leu	Leu	Ala	Val	Tyr	Asp	Arg	Ser	Asn	Thr	Gln
				325					330					335	
Val	Arg	Ala	Phe	Thr	Tyr	Asp	Ala	Gln	His	Pro	Gly	Arg	Met	Val	Ala
			340					345					350		
His	Arg	Tyr	Ala	Gly	Arg	Pro	Glu	Met	Arg	Tyr	Arg	Tyr	Asp	Asp	Thr
		355					360					365			
Gly	Arg	Val	Val	Glu	Gln	Leu	Asn	Pro	Ala	Gly	Leu	Ser	Tyr	Arg	Tyr
	370					375					380				
Leu	Tyr	Glu	Gln	Asp	Arg	Ile	Thr	Val	Thr	Asp	Ser	Leu	Asn	Arg	Arg
385					390					395					400
Glu	Val	Leu	His	Thr	Glu	Gly	Gly	Ala	Gly	Leu	Lys	Arg	Val	Val	Lys
			405						410					415	
Lys	Glu	Leu	Ala	Asp	Gly	Ser	Val	Thr	Arg	Ser	Gly	Tyr	Asp	Ala	Ala
			420					425					430		
Gly	Arg	Leu	Thr	Ala	Gln	Thr	Asp	Ala	Ala	Gly	Arg	Arg	Thr	Glu	Tyr
		435					440					445			
Gly	Leu	Asn	Val	Val	Ser	Gly	Asp	Ile	Thr	Asp	Ile	Thr	Thr	Pro	Asp
	450					455					460				
Gly	Arg	Glu	Thr	Lys	Phe	Tyr	Tyr	Asn	Asp	Gly	Asn	Gln	Leu	Thr	Ala
465					470					475					480
Val	Val	Ser	Pro	Asp	Gly	Leu	Glu	Ser	Arg	Arg	Glu	Tyr	Asp	Glu	Pro
			485						490					495	
Gly	Arg	Leu	Val	Ser	Glu	Thr	Ser	Arg	Ser	Gly	Glu	Thr	Val	Arg	Tyr
		500					505						510		
Arg	Tyr	Asp	Asp	Ala	His	Ser	Glu	Leu	Pro	Ala	Thr	Thr	Thr	Asp	Ala
		515					520						525		
Thr	Gly	Ser	Thr	Arg	Gln	Met	Thr	Trp	Ser	Arg	Tyr	Gly	Gln	Leu	Leu
	530					535					540				
Ala	Phe	Thr	Asp	Cys	Ser	Gly	Tyr	Gln	Thr	Arg	Tyr	Glu	Tyr	Asp	Arg
545					550					555					560
Phe	Gly	Gln	Met	Thr	Ala	Val	His	Arg	Glu	Glu	Gly	Ile	Ser	Leu	Tyr
			565						570					575	
Arg	Arg	Tyr	Asp	Asn	Arg	Gly	Arg	Leu	Thr	Ser	Val	Lys	Asp	Ala	Gln
			580					585					590		
Gly	Arg	Glu	Thr	Arg	Tyr	Glu	Tyr	Asn	Ala	Ala	Gly	Asp	Leu	Thr	Ala

Thr Val Tyr Glu Pro Gly Ser Phe Thr Pro Leu Ile Arg Val Glu Thr
 1060 1065 1070
 Glu Asn Gly Glu Arg Glu Lys Ala Gln Arg Arg Ser Leu Ala Glu Thr
 1075 1080 1085
 Leu Gln Gln Glu Gly Ser Glu Asn Gly His Gly Val Val Phe Pro Ala
 1090 1095 1100
 Glu Leu Val Arg Leu Leu Asp Arg Leu Glu Glu Glu Ile Arg Ala Asp
 1105 1110 1115 1120
 Arg Val Ser Ser Glu Ser Arg Ala Trp Leu Ala Gln Cys Gly Leu Thr
 1125 1130 1135
 Val Glu Gln Leu Ala Arg Gln Val Glu Pro Glu Tyr Thr Pro Ala Arg
 1140 1145 1150
 Lys Ala His Leu Tyr His Cys Asp His Arg Gly Leu Pro Leu Ala Leu
 1155 1160 1165
 Ile Ser Glu Asp Gly Asn Thr Ala Trp Ser Ala Glu Tyr Asp Glu Trp
 1170 1175 1180
 Gly Asn Gln Leu Asn Glu Glu Asn Pro His His Val Tyr Gln Pro Tyr
 1185 1190 1195 1200
 Arg Leu Pro Gly Gln Gln His Asp Glu Glu Ser Gly Leu Tyr Tyr Asn
 1205 1210 1215
 Arg His Arg Tyr Tyr Asp Pro Leu Gln Gly Arg Tyr Ile Thr Gln Asp
 1220 1225 1230
 Pro Met Gly Leu Lys Gly Gly Trp Asn Leu Tyr Gln Tyr Pro Leu Asn
 1235 1240 1245
 Pro Leu Gln Gln Ile Asp Pro Met Gly Leu Leu Gln Thr Trp Asp Asp
 1250 1255 1260
 Ala Arg Ser Gly Ala Cys Thr Gly Gly Val Cys Gly Val Leu Ser Arg
 1265 1270 1275 1280
 Ile Ile Gly Pro Ser Lys Phe Asp Ser Thr Ala Asp Ala Ala Leu Asp
 1285 1290 1295
 Ala Leu Lys Glu Thr Gln Asn Arg Ser Leu Cys Asn Asp Met Glu Tyr
 1300 1305 1310
 Ser Gly Ile Val Cys Lys Asp Thr Asn Gly Lys Tyr Phe Ala Ser Lys
 1315 1320 1325
 Ala Glu Thr Asp Asn Leu Arg Lys Glu Ser Tyr Pro Leu Lys Arg Lys
 1330 1335 1340
 Cys Pro Thr Gly Thr Asp Arg Val Ala Ala Tyr His Thr His Gly Ala
 1345 1350 1355 1360
 Asp Ser His Gly Asp Tyr Val Asp Glu Phe Phe Ser Ser Ser Asp Lys
 1365 1370 1375
 Asn Leu Val Arg Ser Lys Asp Asn Asn Leu Glu Ala Phe Tyr Leu Ala
 1380 1385 1390
 Thr Pro Asp Gly Arg Phe Glu Ala Leu Asn Asn Lys Gly Glu Tyr Ile
 1395 1400 1405
 Phe Ile Arg Asn Ser Val Pro Gly Leu Ser Ser Val Cys Ile Pro Tyr
 1410 1415 1420
 His Asp
 1425

<210> 341

<211> 122

<212> PRT

<213> E. Coli

<400> 341

Met Lys Tyr Ser Ser Ile Phe Ser Met Leu Ser Phe Phe Ile Leu Phe

<212> PRT
<213> E. Coli

<400> 343

Met	Leu	Ala	Ile	Ser	Ser	Asn	Leu	Ser	Lys	Met	Ile	Ile	Phe	Ile	Phe
1				5					10					15	
Ala	Ile	Ile	Ile	Ile	Val	Val	Leu	Cys	Val	Ile	Thr	Tyr	Leu	Tyr	Leu
			20					25					30		
Tyr	Lys	Asp	Glu	Ser	Leu	Val	Ser	Lys	His	Tyr	Ile	Asn	Tyr	Met	Ala
		35					40					45			
Ile	Pro	Glu	Asn	Asp	Gly	Val	Phe	Thr	Trp	Leu	Pro	Asp	Phe	Phe	Pro
	50					55					60				
His	Val	Ala	Val	Asp	Ile	Ser	Ile	Tyr	Thr	Asn	Val	Glu	Asp	Asp	Tyr
65					70					75					80
Phe	Phe	Leu	Ile	Phe	Pro										
					85										

<210> 344

<211> 63

<212> PRT

<213> E. Coli

<400> 344

Met	Arg	Ala	Arg	Glu	Gln	Val	Ala	Lys	Ile	Val	Ser	Lys	Asn	Asp	Pro
1				5					10					15	
Asp	Thr	Lys	Lys	Val	Trp	Cys	Lys	Tyr	Gly	Lys	Ile	Pro	Gly	Gln	Gly
			20					25					30		
Asp	Gly	Val	Asn	Leu	Phe	Phe	Val	Gly	Glu	Ile	Asn	Val	Thr	His	Tyr
		35					40					45			
Phe	Ile	Thr	Asn	Ile	Gly	Ala	Gly	Leu	Pro	Asp	Ala	Cys	Ala	Glu	
	50					55					60				

<210> 345

<211> 167

<212> PRT

<213> E. Coli

<400> 345

Met	Pro	Gly	Asn	Ser	Pro	His	Tyr	Gly	Arg	Trp	Pro	Gln	His	Asp	Phe
1				5					10					15	
Thr	Ser	Leu	Lys	Lys	Leu	Arg	Pro	Gln	Ser	Val	Thr	Ser	Arg	Ile	Gln
			20					25					30		
Pro	Gly	Ser	Asp	Val	Ile	Val	Cys	Ala	Glu	Met	Asp	Glu	Gln	Trp	Gly
		35					40					45			
Tyr	Val	Gly	Ala	Lys	Ser	Arg	Gln	Arg	Trp	Leu	Phe	Tyr	Ala	Tyr	Asp
	50					55					60				
Ser	Leu	Arg	Lys	Thr	Val	Val	Ala	His	Val	Phe	Gly	Glu	Arg	Thr	Met
65					70					75					80
Ala	Thr	Leu	Gly	Arg	Leu	Met	Ser	Leu	Leu	Ser	Pro	Phe	Asp	Val	Val
					85				90					95	
Ile	Trp	Met	Thr	Asp	Gly	Trp	Pro	Leu	Tyr	Glu	Ser	Arg	Leu	Lys	Gly
			100					105					110		
Lys	Leu	His	Val	Ile	Ser	Lys	Arg	Tyr	Thr	Gln	Arg	Ile	Glu	Arg	His

		115					120				125				
Asn	Leu	Asn	Leu	Arg	Gln	His	Leu	Ala	Arg	Leu	Gly	Arg	Lys	Ser	Leu
	130					135					140				
Ser	Phe	Ser	Lys	Ser	Val	Glu	Leu	His	Asp	Lys	Val	Ile	Gly	His	Tyr
145					150					155					160
Leu	Asn	Ile	Lys	His	Tyr	Gln									
				165											

<210> 346
 <211> 91
 <212> PRT
 <213> E. Coli

Met	Ala	Ser	Val	Ser	Ile	Ser	Cys	Pro	Ser	Cys	Ser	Ala	Thr	Asp	Gly
1				5					10					15	
Val	Val	Arg	Asn	Gly	Lys	Ser	Thr	Ala	Gly	His	Gln	Arg	Tyr	Leu	Cys
			20					25					30		
Ser	His	Cys	Arg	Lys	Thr	Trp	Gln	Leu	Gln	Phe	Thr	Tyr	Thr	Ala	Ser
		35					40					45			
Gln	Pro	Gly	Thr	His	Gln	Lys	Ile	Ile	Asp	Met	Ala	Met	Asn	Gly	Val
	50					55					60				
Gly	Cys	Arg	Ala	Thr	Ala	Arg	Ile	Met	Gly	Val	Gly	Leu	Asn	Thr	Ile
65					70					75					80
Leu	Arg	His	Leu	Lys	Asn	Ser	Gly	Arg	Ser	Arg					
				85					90						

<210> 347
 <211> 138
 <212> PRT
 <213> E. Coli

Met	Met	Thr	Lys	Thr	Gln	Ile	Asn	Lys	Leu	Ile	Lys	Met	Met	Asn	Asp
1				5					10					15	
Leu	Asp	Tyr	Pro	Phe	Glu	Ala	Pro	Leu	Lys	Glu	Ser	Phe	Ile	Glu	Ser
			20					25					30		
Ile	Ile	Gln	Ile	Glu	Phe	Asn	Ser	Asn	Ser	Thr	Asn	Cys	Leu	Glu	Lys
		35					40					45			
Leu	Cys	Asn	Glu	Val	Ser	Ile	Leu	Phe	Lys	Asn	Gln	Pro	Asp	Tyr	Leu
	50					55					60				
Thr	Phe	Leu	Arg	Ala	Met	Asp	Gly	Phe	Glu	Val	Asn	Gly	Leu	Arg	Leu
65					70					75					80
Phe	Ser	Leu	Ser	Ile	Pro	Glu	Pro	Ser	Val	Lys	Asn	Leu	Phe	Ala	Val
				85					90					95	
Asn	Glu	Phe	Tyr	Arg	Asn	Asn	Asp	Asp	Phe	Ile	Asn	Pro	Asp	Leu	Gln
			100				105						110		
Glu	Arg	Leu	Val	Ile	Gly	Asp	Tyr	Ser	Ile	Ser	Ile	Phe	Thr	Tyr	Asp
		115					120					125			
Ile	Lys	Gly	Asp	Ala	Ala	Asn	Leu	Leu	Ile						
	130					135									

<210> 348

<211> 392
 <212> PRT
 <213> E. Coli

<400> 348

Met	Ser	Asn	Ile	Val	Tyr	Leu	Thr	Val	Thr	Gly	Glu	Gln	Gln	Gly	Ser
1			5					10						15	
Ile	Ser	Ala	Gly	Cys	Gly	Thr	Ser	Glu	Ser	Thr	Gly	Asn	Arg	Trp	Gln
		20					25					30			
Ser	Gly	His	Glu	Asp	Glu	Ile	Phe	Thr	Phe	Ser	Leu	Leu	Asn	Asn	Ile
	35					40					45				
Asn	Asn	Thr	Gly	Leu	Gly	Ser	Gln	Phe	His	Gly	Ile	Thr	Phe	Cys	Lys
50					55					60					
Leu	Ile	Asp	Lys	Ser	Thr	Pro	Leu	Phe	Ile	Asn	Ser	Ile	Asn	Asn	Asn
65				70					75					80	
Glu	Gln	Leu	Phe	Met	Gly	Phe	Asp	Phe	Tyr	Arg	Ile	Asn	Arg	Phe	Gly
			85					90						95	
Arg	Leu	Glu	Lys	Tyr	Tyr	Tyr	Ile	Gln	Leu	Arg	Gly	Ala	Phe	Leu	Ser
			100				105					110			
Ala	Ile	His	His	Gln	Ile	Ile	Glu	Asn	Gln	Leu	Asp	Thr	Glu	Thr	Ile
	115					120						125			
Thr	Ile	Ser	Tyr	Glu	Phe	Ile	Leu	Cys	Gln	His	Leu	Ile	Ala	Asn	Thr
130						135					140				
Glu	Phe	Ser	Tyr	Leu	Ala	Leu	Pro	Glu	Asn	Tyr	Asn	Arg	Leu	Phe	Leu
145				150					155					160	
Pro	Asn	Ser	Lys	Asn	Gln	Thr	Asn	Asn	Arg	Phe	Lys	Thr	Leu	Asn	Ser
			165				170						175		
Lys	Ala	Ile	Gly	Arg	Leu	Leu	Ala	Ala	Gly	Gly	Val	Tyr	Asn	Gly	Asn
	180					185						190			
Ile	Glu	Gly	Phe	Arg	Asp	Thr	Ala	Glu	Lys	Leu	Gly	Gly	Asp	Ala	Ile
	195					200					205				
Lys	Gly	Tyr	Asp	Gln	Ile	Leu	Asn	Glu	Lys	Thr	Ala	Gly	Ile	Ala	Ile
210				215						220					
Ala	Thr	Ala	Ser	Ile	Leu	Leu	Thr	Lys	Arg	Ser	Asn	Val	Asp	Thr	Tyr
225				230					235					240	
Thr	Glu	Ile	Asn	Ser	Tyr	Leu	Gly	Lys	Leu	Arg	Gly	Gln	Gln	Lys	Leu
			245					250						255	
Leu	Asp	Gly	Ile	Asp	Ile	Ile	Glu	Ile	Ile	Tyr	Ile	Lys	Arg	Pro	Ser
	260					265						270			
Lys	Asp	Leu	Ala	Asn	Leu	Arg	Lys	Glu	Phe	Asn	Lys	Thr	Val	Arg	Lys
	275				280						285				
Asn	Phe	Leu	Ile	Lys	Leu	Ala	Lys	Thr	Ser	Glu	Ala	Ser	Gly	Arg	Phe
290					295					300					
Asn	Ala	Glu	Asp	Leu	Leu	Arg	Met	Arg	Lys	Gly	Asn	Val	Pro	Leu	Asn
305				310					315					320	
Tyr	Asn	Val	His	His	Lys	Leu	Ser	Leu	Asp	Asp	Gly	Gly	Thr	Asn	Asp
			325					330					335		
Phe	Glu	Asn	Leu	Val	Leu	Ile	Glu	Asn	Glu	Pro	Tyr	His	Lys	Val	Phe
	340					345						350			
Thr	Asn	Met	Gln	Ser	Arg	Ile	Ala	Lys	Gly	Ile	Leu	Val	Gly	Glu	Ser
	355					360						365			
Lys	Ile	Thr	Pro	Trp	Ala	Ile	Pro	Ser	Gly	Ser	Ile	Tyr	Pro	Pro	Met
370					375						380				
Lys	Asn	Ile	Met	Asp	His	Thr	Lys								
385				390											

<210> 349
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 <212> PRT
 <213> E. Coli

<400> 349

Met	Val	Leu	Ala	Leu	Asn	Tyr	Asn	Met	His	Gly	Val	Asn	Ile	Arg	Ser
1				5					10					15	
Glu	Asn	Ala	Ala	Lys	Pro	His	Thr	Met	Pro	Ser	Arg	Tyr	Leu	Cys	Glu
		20						25					30		
Tyr	Ile	Arg	Ser	Ile	Glu	Lys	Asn	Gly	His	Ala	Leu	Asp	Phe	Gly	Cys
		35					40					45			
Gly	Lys	Leu	Arg	Tyr	Ser	Asp	Glu	Leu	Ile	Ser	Lys	Phe	Asp	Glu	Val
	50					55					60				
Thr	Phe	Leu	Asp	Ser	Lys	Arg	Gln	Leu	Glu	Arg	Glu	Gln	Ile	Ile	Arg
65					70					75					80
Gly	Ile	Lys	Thr	Lys	Ile	Ile	Asp	Tyr	Val	Pro	Arg	Tyr	Tyr	Lys	Asn
				85					90					95	
Ala	Asn	Thr	Val	Ala	Phe	Glu	Asp	Val	Asp	Lys	Ile	Ile	Gly	Gly	Tyr
			100					105					110		
Asp	Phe	Ile	Leu	Cys	Ser	Asn	Val	Leu	Ser	Ala	Val	Pro	Cys	Arg	Asp
		115					120					125			
Thr	Ile	Asp	Lys	Ile	Val	Leu	Ser	Ile	Lys	Arg	Leu	Leu	Lys	Ser	Gly
	130					135						140			
Gly	Glu	Thr	Leu	Ile	Val	Asn	Gln	Tyr	Lys	Ser	Ser	Tyr	Phe	Lys	Lys
145					150					155					160
Tyr	Glu	Thr	Gly	Arg	Lys	His	Leu	Tyr	Gly	Tyr	Ile	Tyr	Lys	Asn	Ser
			165						170					175	
Lys	Ser	Val	Ser	Tyr	Tyr	Gly	Leu	Leu	Asp	Glu	Leu	Ala	Val	Gln	Glu
			180					185					190		
Ile	Cys	Ser	Ser	His	Gly	Leu	Glu	Ile	Leu	Lys	Ser	Trp	Ser	Lys	Ala
		195					200					205			
Gly	Ser	Ser	Tyr	Val	Thr	Val	Gly	Ser	Cys	Asn	Ala	Ile			
	210					215					220				

<210> 350
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 <212> PRT
 <213> E. Coli

<400> 350

Met	Asn	Asn	Met	Phe	Glu	Pro	Pro	Lys	Asn	Tyr	Asn	Glu	Met	Leu	Pro
1				5					10					15	
Lys	Leu	His	Lys	Ala	Thr	Phe	Leu	Asn	Thr	Leu	Ile	Tyr	Cys	Ile	Leu
			20					25					30		
Leu	Val	Ile	Tyr	Glu	Tyr	Ile	Pro	Leu	Ile	Thr	Leu	Pro	Thr	Lys	Tyr
		35					40					45			
Val	Pro	Pro	Ile	Lys	Asp	His	Glu	Ser	Phe	Ile	Asn	Trp	Ala	Leu	Ser
	50					55					60				
Phe	Gly	Ile	Leu	Pro	Cys	Ala	Phe	Ala	Ile	Phe	Ala	Tyr	Leu	Ile	Ser
65					70					75					80
Gly	Ala	Leu	Asp	Leu	His	Asn	Asn	Ala	Ala	Lys	Leu	Leu	Arg	Val	Arg
				85					90					95	
Tyr	Leu	Trp	Asp	Lys	His	Leu	Ile	Ile	Lys	Pro	Leu	Ser	Arg	Arg	Ala
			100					105					110		

Gly	Val	Asn	Arg	Lys	Leu	Asn	Lys	Asp	Glu	Ala	His	Asn	Val	Met	Ser
		115					120					125			
Asn	Leu	Tyr	Tyr	Pro	Glu	Val	Arg	Lys	Ile	Glu	Asp	Lys	His	Tyr	Ile
		130					135					140			
Glu	Leu	Phe	Trp	Asn	Lys	Val	Tyr	Tyr	Phe	Trp	Ile	Phe	Phe	Glu	Phe
145					150					155					160
Ser	Ile	Ile	Ala	Leu	Ile	Ser	Phe	Leu	Ile	Ile	Phe	Phe	Cys	Lys	Gln
				165					170					175	
Met	Asp	Ile	Phe	His	Val	Glu	Gly	Ser	Leu	Leu	Ser	Leu	Phe	Phe	Phe
			180					185					190		
Val	Ile	Leu	Ser	Phe	Ser	Val	Ser	Gly	Ile	Ile	Phe	Ala	Leu	Thr	Val
		195					200					205			
Lys	Pro	Arg	Thr	Glu	Ser	Gln	Val	Gly	Lys	Ile	Pro	Asp	Asp	Lys	Ile
		210				215					220				
Lys	Glu	Phe	Phe	Thr	Lys	Asn	Asn	Ile	Asn						
225					230										

<210> 351
 <211> 94
 <212> PRT
 <213> E. Coli

<400> 351															
Met	Phe	Thr	Ile	Asn	Ala	Glu	Val	Arg	Lys	Glu	Gln	Gly	Lys	Gly	Ala
1				5					10					15	
Ser	Arg	Arg	Leu	Arg	Ala	Ala	Asn	Lys	Phe	Pro	Ala	Ile	Ile	Tyr	Gly
			20					25					30		
Gly	Lys	Glu	Ala	Pro	Leu	Ala	Ile	Glu	Leu	Asp	His	Asp	Lys	Val	Met
		35					40					45			
Asn	Met	Gln	Ala	Lys	Ala	Glu	Phe	Tyr	Ser	Glu	Val	Leu	Thr	Ile	Val
		50				55					60				
Val	Asp	Gly	Lys	Glu	Ile	Lys	Val	Lys	Ala	Gln	Asp	Val	Gln	Arg	His
65					70					75					80
Pro	Tyr	Lys	Pro	Lys	Leu	Gln	His	Ile	Asp	Phe	Val	Arg	Ala		
				85					90						

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 <213> E. Coli

<400> 352															
Met	Val	Leu	Phe	Tyr	Arg	Ala	His	Trp	Arg	Asp	Tyr	Lys	Asn	Asp	Gln
1				5					10					15	
Val	Arg	Ile	Met	Met	Asn	Leu	Thr	Thr	Leu	Thr	His	Arg	Asp	Ala	Leu
			20					25					30		
Cys	Leu	Asn	Ala	Arg	Phe	Thr	Ser	Arg	Glu	Glu	Ala	Ile	His	Ala	Leu
		35					40					45			
Thr	Gln	Arg	Leu	Ala	Ala	Leu	Gly	Lys	Ile	Ser	Ser	Thr	Glu	Gln	Phe
		50				55					60				
Leu	Glu	Glu	Val	Tyr	Arg	Arg	Glu	Ser	Leu	Gly	Pro	Thr	Ala	Leu	Gly
65					70					75					80
Glu	Gly	Leu	Ala	Val	Pro	His	Gly	Lys	Thr	Ala	Ala	Val	Lys	Glu	Ala
				85					90					95	

Ala	Phe	Ala	Val	Ala	Thr	Leu	Ser	Glu	Pro	Leu	Gln	Trp	Glu	Gly	Val
			100					105					110		
Asp	Gly	Pro	Glu	Ala	Val	Asp	Leu	Val	Val	Leu	Leu	Ala	Ile	Pro	Pro
		115					120					125			
Asn	Glu	Ala	Gly	Thr	Thr	His	Met	Gln	Leu	Leu	Thr	Ala	Leu	Thr	Thr
	130					135					140				
Arg	Leu	Ala	Asp	Asp	Glu	Ile	Arg	Ala	Arg	Ile	Gln	Ser	Ala	Thr	Thr
145					150					155					160
Pro	Asp	Glu	Leu	Leu	Ser	Ala	Leu	Asp	Asp	Lys	Gly	Gly	Thr	Gln	Pro
			165					170						175	
Ser	Ala	Ser	Phe	Ser	Asn	Ala	Pro	Thr	Ile	Val	Cys	Val	Thr	Ala	Cys
		180						185					190		
Pro	Ala	Gly	Ile	Ala	His	Thr	Tyr	Met	Ala	Ala	Glu	Tyr	Leu	Glu	Lys
	195						200				205				
Ala	Gly	Arg	Lys	Leu	Gly	Val	Asn	Val	Tyr	Val	Glu	Lys	Gln	Gly	Ala
	210					215					220				
Asn	Gly	Ile	Glu	Gly	Arg	Leu	Thr	Ala	Asp	Gln	Leu	Asn	Ser	Ala	Thr
225					230					235					240
Ala	Cys	Ile	Phe	Ala	Ala	Glu	Val	Ala	Ile	Lys	Glu	Ser	Glu	Arg	Phe
				245					250					255	
Asn	Gly	Ile	Pro	Ala	Leu	Ser	Val	Pro	Val	Ala	Glu	Pro	Ile	Arg	His
			260					265					270		
Ala	Glu	Ala	Leu	Ile	Gln	Gln	Ala	Leu	Thr	Leu	Lys	Arg	Ser	Asp	Glu
	275						280					285			
Thr	Arg	Thr	Val	Gln	Gln	Asp	Thr	Gln	Pro	Val	Lys	Ser	Val	Lys	Thr
	290					295					300				
Glu	Leu	Lys	Gln	Ala	Leu	Leu	Ser	Gly	Ile	Ser	Phe	Ala	Val	Pro	Leu
305					310					315					320
Ile	Val	Ala	Gly	Gly	Thr	Val	Leu	Ala	Val	Ala	Val	Leu	Leu	Ser	Gln
				325					330					335	
Ile	Phe	Gly	Leu	Gln	Asp	Leu	Phe	Asn	Glu	Glu	Asn	Ser	Trp	Leu	Trp
		340						345					350		
Met	Tyr	Arg	Lys	Leu	Gly	Gly	Gly	Leu	Leu	Gly	Ile	Leu	Met	Val	Pro
	355					360						365			
Val	Leu	Ala	Ala	Tyr	Thr	Ala	Tyr	Ser	Leu	Ala	Asp	Lys	Pro	Ala	Leu
	370					375					380				
Ala	Pro	Gly	Phe	Ala	Ala	Gly	Leu	Ala	Ala	Asn	Met	Ile	Gly	Ser	Gly
385					390					395					400
Phe	Leu	Gly	Ala	Val	Val	Gly	Gly	Leu	Ile	Ala	Gly	Tyr	Leu	Met	Arg
				405					410					415	
Trp	Val	Lys	Asn	His	Leu	Arg	Leu	Ser	Ser	Lys	Phe	Asn	Gly	Phe	Leu
			420					425					430		
Thr	Phe	Tyr	Leu	Tyr	Pro	Val	Leu	Gly	Thr	Leu	Gly	Ala	Gly	Ser	Leu
		435					440					445			
Met	Leu	Phe	Val	Val	Gly	Glu	Pro	Val	Ala	Trp	Ile	Asn	Asn	Ser	Leu
	450					455					460				
Thr	Ala	Trp	Leu	Asn	Gly	Leu	Ser	Gly	Ser	Asn	Ala	Leu	Leu	Leu	Gly
465					470					475					480
Ala	Ile	Leu	Gly	Phe	Met	Cys	Ser	Phe	Asp	Leu	Gly	Gly	Pro	Val	Asn
				485					490					495	
Lys	Ala	Ala	Tyr	Ala	Phe	Cys	Leu	Gly	Ala	Met	Ala	Asn	Gly	Val	Tyr
			500					505					510		
Gly	Pro	Tyr	Ala	Ile	Phe	Ala	Ser	Val	Lys	Met	Val	Ser	Ala	Phe	Thr
		515					520					525			
Val	Thr	Ala	Ser	Thr	Met	Leu	Ala	Pro	Arg	Leu	Phe	Lys	Glu	Phe	Glu
	530					535					540				
Ile	Glu	Thr	Gly	Lys	Ser	Thr	Trp	Leu	Leu	Gly	Leu	Ala	Gly	Ile	Thr

545					550					555				560	
Glu	Gly	Ala	Ile	Pro	Met	Ala	Ile	Glu	Asp	Pro	Leu	Arg	Val	Ile	Gly
				565					570					575	
Ser	Phe	Val	Leu	Gly	Ser	Met	Val	Thr	Gly	Ala	Ile	Val	Gly	Ala	Met
			580					585					590		
Asn	Ile	Gly	Leu	Ser	Thr	Pro	Gly	Ala	Gly	Ile	Phe	Ser	Leu	Phe	Leu
		595					600					605			
Leu	His	Asp	Asn	Gly	Ala	Gly	Gly	Val	Met	Ala	Ala	Ile	Gly	Trp	Phe
	610					615					620				
Gly	Ala	Ala	Leu	Val	Gly	Ala	Ala	Ile	Ser	Thr	Ala	Ile	Leu	Leu	Met
625					630					635					640
Trp	Arg	Arg	His	Ala	Val	Lys	His	Gly	Asn	Tyr	Leu	Thr	Asp	Gly	Val
				645					650					655	
Met	Pro														

<210> 353
 <211> 877
 <212> PRT
 <213> E. Coli

<400> 353

Met	Lys	Ala	Val	Ser	Arg	Val	His	Ile	Thr	Pro	His	Met	His	Trp	Asp
1				5					10					15	
Arg	Glu	Trp	Tyr	Phe	Thr	Thr	Glu	Glu	Ser	Arg	Ile	Leu	Leu	Val	Asn
			20					25					30		
Asn	Met	Glu	Glu	Ile	Leu	Cys	Arg	Leu	Glu	Gln	Asp	Asn	Glu	Tyr	Lys
		35				40						45			
Tyr	Tyr	Val	Leu	Asp	Gly	Gln	Thr	Ala	Ile	Leu	Glu	Asp	Tyr	Phe	Ala
	50					55					60				
Val	Lys	Pro	Glu	Asn	Lys	Asp	Arg	Val	Lys	Lys	Gln	Val	Glu	Ala	Gly
65				70						75					80
Lys	Leu	Ile	Ile	Gly	Pro	Trp	Tyr	Thr	Gln	Thr	Asp	Thr	Thr	Ile	Val
				85					90					95	
Ser	Ala	Glu	Ser	Ile	Val	Arg	Asn	Leu	Met	Tyr	Gly	Met	Arg	Asp	Cys
			100					105					110		
Leu	Ala	Phe	Gly	Glu	Pro	Met	Lys	Ile	Gly	Tyr	Leu	Pro	Asp	Ser	Phe
		115					120					125			
Gly	Met	Ser	Gly	Gln	Leu	Pro	His	Ile	Tyr	Asn	Gly	Phe	Gly	Ile	Thr
	130					135					140				
Arg	Thr	Met	Phe	Trp	Arg	Gly	Cys	Ser	Glu	Arg	His	Gly	Thr	Asp	Lys
145				150						155					160
Thr	Glu	Phe	Leu	Trp	Gln	Ser	Ser	Asp	Gly	Ser	Glu	Val	Thr	Ala	Gln
				165					170					175	
Val	Leu	Pro	Leu	Gly	Tyr	Ala	Ile	Gly	Lys	Tyr	Leu	Pro	Ala	Asp	Glu
			180					185					190		
Asn	Gly	Leu	Arg	Lys	Arg	Leu	Asp	Ser	Tyr	Phe	Asp	Val	Leu	Glu	Lys
		195					200					205			
Ala	Ser	Val	Thr	Lys	Glu	Ile	Leu	Leu	Pro	Asn	Gly	His	Asp	Gln	Met
	210					215					220				
Pro	Leu	Gln	Gln	Asn	Ile	Phe	Glu	Val	Met	Asp	Lys	Leu	Arg	Glu	Ile
225				230						235					240
Tyr	Pro	Gln	Arg	Lys	Phe	Val	Met	Ser	Arg	Phe	Glu	Glu	Val	Phe	Glu
				245					250					255	
Lys	Ile	Glu	Ala	Gln	Arg	Asp	Asn	Leu	Ala	Thr	Leu	Lys	Gly	Glu	Phe
			260					265					270		

Ile	Asp	Gly	Lys	Tyr	Met	Arg	Val	His	Arg	Thr	Ile	Gly	Ser	Thr	Arg
	275						280					285			
Met	Asp	Ile	Lys	Ile	Ala	His	Ala	Arg	Ile	Glu	Asn	Lys	Ile	Val	Asn
	290					295					300				
Leu	Leu	Glu	Pro	Leu	Ala	Thr	Leu	Ala	Trp	Thr	Leu	Gly	Phe	Glu	Tyr
305					310					315					320
His	His	Gly	Leu	Leu	Glu	Lys	Met	Trp	Lys	Glu	Ile	Leu	Lys	Asn	His
			325						330					335	
Ala	His	Asp	Ser	Ile	Gly	Cys	Cys	Cys	Ser	Asp	Lys	Val	His	Arg	Glu
			340					345					350		
Ile	Val	Ala	Arg	Phe	Glu	Leu	Ala	Glu	Asp	Met	Ala	Asp	Asn	Leu	Ile
		355					360					365			
Arg	Phe	Tyr	Met	Arg	Lys	Ile	Ala	Asp	Asn	Met	Pro	Gln	Ser	Asp	Ala
	370				375						380				
Asp	Lys	Leu	Val	Leu	Phe	Asn	Leu	Met	Pro	Trp	Pro	Arg	Glu	Glu	Val
385				390						395					400
Ile	Asn	Thr	Thr	Val	Arg	Leu	Arg	Ala	Ser	Gln	Phe	Asn	Leu	Arg	Asp
				405					410					415	
Asp	Arg	Gly	Gln	Pro	Val	Pro	Tyr	Phe	Ile	Arg	His	Ala	Arg	Glu	Ile
			420					425					430		
Asp	Pro	Gly	Leu	Ile	Asp	Arg	Gln	Ile	Val	His	Tyr	Gly	Asn	Tyr	Asp
		435					440					445			
Pro	Phe	Met	Glu	Phe	Asp	Ile	Gln	Ile	Asn	Gln	Ile	Val	Pro	Ser	Met
	450					455						460			
Gly	Tyr	Arg	Thr	Leu	Tyr	Ile	Glu	Ala	Asn	Gln	Pro	Gly	Asn	Val	Ile
465				470						475					480
Ala	Ala	Lys	Ser	Asp	Ala	Glu	Gly	Ile	Leu	Glu	Asn	Ala	Phe	Trp	Gln
			485						490					495	
Ile	Ala	Leu	Asn	Glu	Asp	Gly	Ser	Leu	Gln	Leu	Val	Asp	Lys	Asp	Ser
			500					505					510		
Gly	Val	Arg	Tyr	Asp	Arg	Val	Leu	Gln	Ile	Glu	Glu	Ser	Ser	Asp	Asp
		515					520					525			
Gly	Asp	Glu	Tyr	Asp	Tyr	Ser	Pro	Ala	Lys	Glu	Glu	Trp	Val	Ile	Thr
	530					535						540			
Ala	Ala	Asn	Ala	Lys	Pro	Gln	Cys	Asp	Ile	Ile	His	Glu	Ala	Trp	Gln
545					550					555					560
Ser	Arg	Ala	Val	Ile	Arg	Tyr	Asp	Met	Ala	Val	Pro	Leu	Asn	Leu	Ser
				565					570					575	
Glu	Arg	Ser	Ala	Arg	Gln	Ser	Thr	Gly	Arg	Val	Gly	Val	Val	Leu	Val
			580					585					590		
Val	Thr	Leu	Ser	His	Asn	Ser	Arg	Arg	Ile	Asp	Val	Asp	Ile	Asn	Leu
		595					600					605			
Asp	Asn	Gln	Ala	Asp	Asp	His	Arg	Leu	Arg	Val	Leu	Val	Pro	Thr	Pro
	610					615					620				
Phe	Asn	Thr	Asp	Ser	Val	Leu	Ala	Asp	Thr	Gln	Phe	Gly	Ser	Leu	Thr
625					630					635					640
Arg	Pro	Val	Asn	Asp	Ser	Ala	Met	Asn	Asn	Trp	Gln	Gln	Glu	Gly	Trp
			645						650					655	
Lys	Glu	Ala	Pro	Val	Pro	Val	Trp	Asn	Met	Leu	Asn	Tyr	Val	Ala	Leu
			660					665					670		
Gln	Glu	Gly	Arg	Asn	Gly	Met	Ala	Val	Phe	Ser	Glu	Gly	Leu	Arg	Glu
		675					680					685			
Phe	Glu	Val	Ile	Gly	Glu	Glu	Lys	Lys	Thr	Phe	Ala	Ile	Thr	Leu	Leu
	690					695					700				
Arg	Gly	Val	Gly	Leu	Leu	Gly	Lys	Glu	Asp	Leu	Leu	Leu	Arg	Pro	Gly
705				710						715					720
Arg	Pro	Ser	Gly	Ile	Lys	Met	Pro	Val	Pro	Asp	Ser	Gln	Leu	Arg	Gly

				725					730				735			
Leu	Leu	Ser	Cys	Arg	Leu	Ser	Leu	Leu	Ser	Tyr	Thr	Gly	Thr	Pro	Thr	
			740					745					750			
Ala	Ala	Gly	Val	Ala	Gln	Gln	Ala	Arg	Ala	Trp	Leu	Thr	Pro	Val	Gln	
		755					760					765				
Cys	Tyr	Asn	Lys	Ile	Pro	Trp	Asp	Val	Met	Lys	Leu	Asn	Lys	Ala	Gly	
	770					775					780					
Phe	Asn	Val	Pro	Glu	Ser	Tyr	Ser	Leu	Leu	Lys	Met	Pro	Pro	Val	Gly	
785					790					795					800	
Cys	Leu	Ile	Ser	Ala	Leu	Lys	Lys	Ala	Glu	Asp	Arg	Gln	Glu	Val	Ile	
				805					810					815		
Leu	Arg	Leu	Phe	Asn	Pro	Ala	Glu	Ser	Ala	Thr	Cys	Asp	Ala	Thr	Val	
			820					825					830			
Ala	Phe	Ser	Arg	Glu	Val	Ile	Ser	Cys	Ser	Glu	Thr	Met	Met	Asp	Glu	
		835					840					845				
His	Ile	Thr	Thr	Glu	Glu	Asn	Gln	Gly	Ser	Asn	Leu	Ser	Gly	Pro	Phe	
	850					855					860					
Leu	Pro	Gly	Gln	Ser	Arg	Thr	Phe	Ser	Tyr	Arg	Leu	Ala				
865					870					875						

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 <212> PRT
 <213> E. Coli

				<400>												
				354												
Met	Met	Leu	Asp	Ile	Val	Glu	Leu	Ser	Arg	Leu	Gln	Phe	Ala	Leu	Thr	
1				5					10					15		
Ala	Met	Tyr	His	Phe	Leu	Phe	Val	Pro	Leu	Thr	Leu	Gly	Met	Ala	Phe	
			20					25					30			
Leu	Leu	Ala	Ile	Met	Glu	Thr	Val	Tyr	Val	Leu	Ser	Gly	Lys	Gln	Ile	
		35					40					45				
Tyr	Lys	Asp	Met	Thr	Lys	Phe	Trp	Gly	Lys	Leu	Phe	Gly	Ile	Asn	Phe	
	50					55					60					
Ala	Leu	Gly	Val	Ala	Thr	Gly	Leu	Thr	Met	Glu	Phe	Gln	Phe	Gly	Thr	
65					70					75					80	
Asn	Trp	Ser	Tyr	Tyr	Ser	His	Tyr	Val	Gly	Asp	Ile	Phe	Gly	Ala	Pro	
				85					90					95		
Leu	Ala	Ile	Glu	Gly	Leu	Met	Ala	Phe	Phe	Leu	Glu	Ser	Thr	Phe	Val	
			100					105					110			
Gly	Leu	Phe	Phe	Phe	Gly	Trp	Asp	Arg	Leu	Gly	Lys	Val	Gln	His	Met	
		115					120					125				
Cys	Val	Thr	Trp	Leu	Val	Ala	Leu	Gly	Ser	Asn	Leu	Ser	Ala	Leu	Trp	
	130					135					140					
Ile	Leu	Val	Ala	Asn	Gly	Trp	Met	Gln	Asn	Pro	Ile	Ala	Ser	Asp	Phe	
145					150					155					160	
Asn	Phe	Glu	Thr	Met	Arg	Met	Glu	Met	Val	Ser	Phe	Ser	Glu	Leu	Val	
				165					170					175		
Leu	Asn	Pro	Val	Ala	Gln	Val	Lys	Phe	Val	His	Thr	Val	Ala	Ser	Gly	
			180					185					190			
Tyr	Val	Thr	Gly	Ala	Met	Phe	Ile	Leu	Gly	Ile	Ser	Ala	Trp	Tyr	Met	
		195					200					205				
Leu	Lys	Gly	Arg	Asp	Phe	Ala	Phe	Ala	Lys	Arg	Ser	Phe	Ala	Ile	Ala	
	210					215					220					
Ala	Ser	Phe	Gly	Met	Ala	Ala	Val	Leu	Ser	Val	Ile	Val	Leu	Gly	Asp	
225					230					235					240	

Glu	Ser	Gly	Tyr	Glu	Met	Gly	Asp	Val	Gln	Lys	Thr	Lys	Leu	Ala	Ala		
				245					250					255			
Ile	Glu	Ala	Glu	Trp	Glu	Thr	Gln	Pro	Ala	Pro	Ala	Ala	Phe	Thr	Leu		
			260					265					270				
Phe	Gly	Ile	Pro	Asp	Gln	Glu	Glu	Glu	Thr	Asn	Lys	Phe	Ala	Ile	Gln		
		275				280						285					
Ile	Pro	Tyr	Ala	Leu	Gly	Ile	Ile	Ala	Thr	Arg	Ser	Val	Asp	Thr	Pro		
	290				295						300						
Val	Ile	Gly	Leu	Lys	Glu	Leu	Met	Val	Gln	His	Glu	Glu	Arg	Ile	Arg		
305					310					315					320		
Asn	Gly	Met	Lys	Ala	Tyr	Ser	Leu	Leu	Glu	Gln	Leu	Arg	Ser	Gly	Ser		
				325					330					335			
Thr	Asp	Gln	Ala	Val	Arg	Asp	Gln	Phe	Asn	Ser	Met	Lys	Lys	Asp	Leu		
			340					345					350				
Gly	Tyr	Gly	Leu	Leu	Leu	Lys	Arg	Tyr	Thr	Pro	Asn	Val	Ala	Asp	Ala		
		355					360					365					
Thr	Glu	Ala	Gln	Ile	Gln	Gln	Ala	Thr	Lys	Asp	Ser	Ile	Pro	Arg	Val		
	370					375					380						
Ala	Pro	Leu	Tyr	Phe	Ala	Phe	Arg	Ile	Met	Val	Ala	Cys	Gly	Phe	Leu		
385					390					395					400		
Leu	Leu	Ala	Ile	Ile	Ala	Leu	Ser	Phe	Trp	Ser	Val	Ile	Arg	Asn	Arg		
				405					410					415			
Ile	Gly	Glu	Lys	Lys	Trp	Leu	Leu	Arg	Ala	Ala	Leu	Tyr	Gly	Ile	Pro		
			420					425					430				
Leu	Pro	Trp	Ile	Ala	Val	Glu	Ala	Gly	Trp	Phe	Val	Ala	Glu	Tyr	Gly		
		435					440					445					
Arg	Gln	Pro	Trp	Ala	Ile	Gly	Glu	Val	Leu	Pro	Thr	Ala	Val	Ala	Asn		
	450					455					460						
Ser	Ser	Leu	Thr	Ala	Gly	Asp	Leu	Ile	Phe	Ser	Met	Val	Leu	Ile	Cys		
465					470					475					480		
Gly	Leu	Tyr	Thr	Leu	Phe	Leu	Val	Ala	Glu	Leu	Phe	Leu	Met	Phe	Lys		
				485					490					495			
Phe	Ala	Arg	Leu	Gly	Pro	Ser	Ser	Leu	Lys	Thr	Gly	Arg	Tyr	His	Phe		
			500					505					510				
Glu	Gln	Ser	Ser	Thr	Thr	Thr	Gln	Pro	Ala	Arg							
		515					520										

<210> 355

<211> 379

<212> PRT

<213> E. Coli

<400> 355

Met	Ile	Asp	Tyr	Glu	Val	Leu	Arg	Phe	Ile	Trp	Trp	Leu	Leu	Val	Gly		
1				5					10					15			
Val	Leu	Leu	Ile	Gly	Phe	Ala	Val	Thr	Asp	Gly	Phe	Asp	Met	Gly	Val		
			20					25					30				
Gly	Met	Leu	Thr	Arg	Phe	Leu	Gly	Arg	Asn	Asp	Thr	Glu	Arg	Arg	Ile		
		35					40					45					
Met	Ile	Asn	Ser	Ile	Ala	Pro	His	Trp	Asp	Gly	Asn	Gln	Val	Trp	Leu		
	50					55					60						
Ile	Thr	Ala	Gly	Gly	Ala	Leu	Phe	Ala	Ala	Trp	Pro	Met	Val	Tyr	Ala		
65					70				75						80		
Ala	Ala	Phe	Ser	Gly	Phe	Tyr	Val	Ala	Met	Ile	Leu	Val	Leu	Ala	Ser		
				85					90					95			
Leu	Phe	Phe	Arg	Pro	Val	Gly	Phe	Asp	Tyr	Arg	Ser	Lys	Ile	Glu	Glu		

			100					105				110			
Thr	Arg	Trp	Arg	Asn	Met	Trp	Asp	Trp	Gly	Ile	Phe	Ile	Gly	Ser	Phe
		115					120					125			
Val	Pro	Pro	Leu	Val	Ile	Gly	Val	Ala	Phe	Gly	Asn	Leu	Leu	Gln	Gly
		130				135					140				
Val	Pro	Phe	Asn	Val	Asp	Glu	Tyr	Leu	Arg	Leu	Tyr	Tyr	Thr	Gly	Asn
145					150					155					160
Phe	Phe	Gln	Leu	Leu	Asn	Pro	Phe	Gly	Leu	Leu	Ala	Gly	Val	Val	Ser
			165					170						175	
Val	Gly	Met	Ile	Ile	Thr	Gln	Gly	Ala	Thr	Tyr	Leu	Gln	Met	Arg	Thr
		180					185						190		
Val	Gly	Glu	Leu	His	Leu	Arg	Thr	Arg	Ala	Thr	Ala	Gln	Val	Ala	Ala
		195					200					205			
Leu	Val	Thr	Leu	Val	Cys	Phe	Ala	Leu	Ala	Gly	Val	Trp	Val	Met	Tyr
		210				215					220				
Gly	Ile	Asp	Gly	Tyr	Val	Val	Lys	Ser	Thr	Met	Asp	His	Tyr	Ala	Ala
225					230					235					240
Ser	Asn	Pro	Leu	Asn	Lys	Glu	Val	Val	Arg	Glu	Ala	Gly	Ala	Trp	Leu
				245					250					255	
Val	Asn	Phe	Asn	Asn	Thr	Pro	Ile	Leu	Trp	Ala	Ile	Pro	Ala	Leu	Gly
			260					265					270		
Val	Val	Leu	Pro	Leu	Leu	Thr	Ile	Leu	Thr	Ala	Arg	Met	Asp	Lys	Ala
		275					280					285			
Ala	Trp	Ala	Phe	Val	Phe	Ser	Ser	Leu	Thr	Leu	Ala	Cys	Ile	Ile	Leu
		290				295					300				
Thr	Ala	Gly	Ile	Ala	Met	Phe	Pro	Phe	Val	Met	Pro	Ser	Ser	Thr	Met
305					310					315					320
Met	Asn	Ala	Ser	Leu	Thr	Met	Trp	Asp	Ala	Thr	Ser	Ser	Gln	Leu	Thr
				325					330					335	
Leu	Asn	Val	Met	Thr	Trp	Val	Ala	Val	Val	Leu	Val	Pro	Ile	Ile	Leu
			340					345					350		
Leu	Tyr	Thr	Ala	Trp	Cys	Tyr	Trp	Lys	Met	Phe	Gly	Arg	Ile	Thr	Lys
		355					360					365			
Glu	Asp	Ile	Glu	Arg	Asn	Thr	His	Ser	Leu	Tyr					
		370				375									

<210> 356

<211> 456

<212> PRT

<213> E. Coli

<400> 356

Met	Glu	Leu	Ser	Ser	Leu	Thr	Ala	Val	Ser	Pro	Val	Asp	Gly	Arg	Tyr
1				5					10					15	
Gly	Asp	Lys	Val	Ser	Ala	Leu	Arg	Gly	Ile	Phe	Ser	Glu	Tyr	Gly	Leu
		20						25					30		
Leu	Lys	Phe	Arg	Val	Gln	Val	Glu	Val	Arg	Trp	Leu	Gln	Lys	Leu	Ala
		35					40					45			
Ala	His	Ala	Ala	Ile	Lys	Glu	Val	Pro	Ala	Phe	Ala	Ala	Asp	Ala	Ile
		50				55					60				
Gly	Tyr	Leu	Asp	Ala	Ile	Val	Ala	Ser	Phe	Ser	Glu	Glu	Asp	Ala	Ala
65					70					75					80
Arg	Ile	Lys	Thr	Ile	Glu	Arg	Thr	Thr	Asn	His	Asp	Val	Lys	Ala	Val
				85					90					95	
Glu	Tyr	Phe	Leu	Lys	Glu	Lys	Val	Ala	Glu	Ile	Pro	Glu	Leu	His	Ala
			100					105					110		

Val	Ser	Glu	Phe	Ile	His	Phe	Ala	Cys	Thr	Ser	Glu	Asp	Ile	Asn	Asn
	115						120					125			
Leu	Ser	His	Ala	Leu	Met	Leu	Lys	Thr	Ala	Arg	Asp	Glu	Val	Ile	Leu
	130						135				140				
Pro	Tyr	Trp	Arg	Gln	Leu	Ile	Asp	Gly	Ile	Lys	Asp	Leu	Ala	Val	Gln
145					150					155					160
Tyr	Arg	Asp	Ile	Pro	Leu	Leu	Ser	Arg	Thr	His	Gly	Gln	Pro	Ala	Thr
				165					170					175	
Pro	Ser	Thr	Ile	Gly	Lys	Glu	Met	Ala	Asn	Val	Ala	Tyr	Arg	Met	Glu
		180						185					190		
Arg	Gln	Tyr	Arg	Gln	Leu	Asn	Gln	Val	Glu	Ile	Leu	Gly	Lys	Ile	Asn
	195						200					205			
Gly	Ala	Val	Gly	Asn	Tyr	Asn	Ala	His	Ile	Ala	Ala	Tyr	Pro	Glu	Val
	210					215				220					
Asp	Trp	His	Gln	Phe	Ser	Glu	Glu	Phe	Val	Thr	Ser	Leu	Gly	Ile	Gln
225					230					235					240
Trp	Asn	Pro	Tyr	Thr	Thr	Gln	Ile	Glu	Pro	His	Asp	Tyr	Ile	Ala	Glu
				245					250					255	
Leu	Phe	Asp	Cys	Val	Ala	Arg	Phe	Asn	Thr	Ile	Leu	Ile	Asp	Phe	Asp
		260						265					270		
Arg	Asp	Val	Trp	Gly	Tyr	Ile	Ala	Leu	Asn	His	Phe	Lys	Gln	Lys	Thr
	275						280					285			
Ile	Ala	Gly	Glu	Ile	Gly	Ser	Ser	Thr	Met	Pro	His	Lys	Val	Asn	Pro
	290					295				300					
Ile	Asp	Phe	Glu	Asn	Ser	Glu	Gly	Asn	Leu	Gly	Leu	Ser	Asn	Ala	Val
305					310					315					320
Leu	Gln	His	Leu	Ala	Ser	Lys	Leu	Pro	Val	Ser	Arg	Trp	Gln	Arg	Asp
			325					330					335		
Leu	Thr	Asp	Ser	Thr	Val	Leu	Arg	Asn	Leu	Gly	Val	Gly	Ile	Gly	Tyr
		340						345				350			
Ala	Leu	Ile	Ala	Tyr	Gln	Ser	Thr	Leu	Lys	Gly	Val	Ser	Lys	Leu	Glu
	355						360				365				
Val	Asn	Arg	Asp	His	Leu	Leu	Asp	Glu	Leu	Asp	His	Asn	Trp	Glu	Val
	370					375					380				
Leu	Ala	Glu	Pro	Ile	Gln	Thr	Val	Met	Arg	Arg	Tyr	Gly	Ile	Glu	Lys
385					390					395					400
Pro	Tyr	Glu	Lys	Leu	Lys	Glu	Leu	Thr	Arg	Gly	Lys	Arg	Val	Asp	Ala
			405					410						415	
Glu	Gly	Met	Lys	Gln	Phe	Ile	Asp	Gly	Leu	Ala	Leu	Pro	Glu	Glu	Glu
		420						425				430			
Lys	Ala	Arg	Leu	Lys	Ala	Met	Thr	Pro	Ala	Asn	Tyr	Ile	Gly	Arg	Ala
	435					440						445			
Ile	Thr	Met	Val	Asp	Glu	Leu	Lys								
	450					455									

<210> 357

<211> 61

<212> PRT

<213> E. Coli

<400> 357

Met	Leu	Ile	Leu	Thr	Arg	Arg	Val	Gly	Glu	Thr	Leu	Met	Ile	Gly	Asp
1				5					10					15	
Glu	Val	Thr	Val	Thr	Val	Leu	Gly	Val	Lys	Gly	Asn	Gln	Val	Arg	Ile
		20					25					30			
Gly	Val	Asn	Ala	Pro	Lys	Glu	Val	Ser	Val	His	Arg	Glu	Glu	Ile	Tyr

		35					40					45			
Gln	Arg	Ile	Gln	Ala	Glu	Lys	Ser	Gln	Gln	Ser	Ser	Tyr			
	50					55					60				

<210> 358
 <211> 93
 <212> RNA
 <213> E. Coli

<400> 358	
ggugaggugg ccgagaggcu gaaggcgcuc ccugcuaag ggaguaugcg gucaaaagcu	60
gcauccgggg uucgaauccc cgccucaccg cca	93

<210> 359
 <211> 200
 <212> PRT
 <213> E. Coli

<400> 359	
Met Lys Asn Lys Ala Asp Asn Lys Lys Arg Asn Phe Leu Thr His Ser	
1 5 10 15	
Glu Ile Glu Ser Leu Leu Lys Ala Ala Asn Thr Gly Pro His Ala Ala	
20 25 30	
Arg Asn Tyr Cys Leu Thr Leu Leu Cys Phe Ile His Gly Phe Arg Ala	
35 40 45	
Ser Glu Ile Cys Arg Leu Arg Ile Ser Asp Ile Asp Leu Lys Ala Lys	
50 55 60	
Cys Ile Tyr Ile His Arg Leu Lys Lys Gly Phe Ser Thr Thr His Pro	
65 70 75 80	
Leu Leu Asn Lys Glu Val Gln Ala Leu Lys Asn Trp Leu Ser Ile Arg	
85 90 95	
Thr Ser Tyr Pro His Ala Glu Ser Glu Trp Val Phe Leu Ser Arg Lys	
100 105 110	
Gly Asn Pro Leu Ser Arg Gln Gln Phe Tyr His Ile Ile Ser Thr Ser	
115 120 125	
Gly Gly Asn Ala Gly Leu Ser Leu Glu Ile His Pro His Met Leu Arg	
130 135 140	
His Ser Cys Gly Phe Ala Leu Ala Asn Met Gly Ile Asp Thr Arg Leu	
145 150 155 160	
Ile Gln Asp Tyr Leu Gly His Arg Asn Ile Arg His Thr Val Trp Tyr	
165 170 175	
Thr Ala Ser Asn Ala Gly Arg Phe Tyr Gly Ile Trp Asp Arg Ala Arg	
180 185 190	
Gly Arg Gln Arg His Ala Val Leu	
195 200	

<210> 360
 <211> 198
 <212> PRT
 <213> E. Coli

<400> 360	
Met Ser Lys Arg Arg Tyr Leu Thr Gly Lys Glu Val Gln Ala Met Met	
1 5 10 15	

Gln	Ala	Val	Cys	Tyr	Gly	Ala	Thr	Gly	Ala	Arg	Asp	Tyr	Cys	Leu	Ile
			20					25					30		
Leu	Leu	Ala	Tyr	Arg	His	Gly	Met	Arg	Ile	Ser	Glu	Leu	Leu	Asp	Leu
		35					40					45			
His	Tyr	Gln	Asp	Leu	Asp	Leu	Asn	Glu	Gly	Arg	Ile	Asn	Ile	Arg	Arg
		50				55					60				
Leu	Lys	Asn	Gly	Phe	Ser	Thr	Val	His	Pro	Leu	Arg	Phe	Asp	Glu	Arg
65					70					75				80	
Glu	Ala	Val	Glu	Arg	Trp	Thr	Gln	Glu	Arg	Ala	Asn	Trp	Lys	Gly	Ala
			85						90					95	
Asp	Arg	Thr	Asp	Ala	Ile	Phe	Ile	Ser	Arg	Arg	Gly	Ser	Arg	Leu	Ser
			100					105					110		
Arg	Gln	Gln	Ala	Tyr	Arg	Ile	Ile	Arg	Asp	Ala	Gly	Ile	Glu	Ala	Gly
		115					120					125			
Thr	Val	Thr	Gln	Thr	His	Pro	His	Met	Leu	Arg	His	Ala	Cys	Gly	Tyr
		130				135					140				
Glu	Leu	Ala	Glu	Arg	Gly	Ala	Asp	Thr	Arg	Leu	Ile	Gln	Asp	Tyr	Leu
145					150					155					160
Gly	His	Arg	Asn	Ile	Arg	His	Thr	Val	Arg	Tyr	Thr	Ala	Ser	Asn	Ala
			165					170						175	
Ala	Arg	Phe	Ala	Gly	Leu	Trp	Glu	Arg	Asn	Asn	Leu	Ile	Asn	Glu	Lys
			180					185					190		
Leu	Lys	Arg	Glu	Glu	Val										
			195												

<210> 361
 <211> 182
 <212> PRT
 <213> E. Coli

<400> 361

Met	Lys	Ile	Lys	Thr	Leu	Ala	Ile	Val	Val	Leu	Ser	Ala	Leu	Ser	Leu
1				5					10					15	
Ser	Ser	Thr	Ala	Ala	Leu	Ala	Ala	Ala	Thr	Thr	Val	Asn	Gly	Gly	Thr
			20					25				30			
Val	His	Phe	Lys	Gly	Glu	Val	Val	Asn	Ala	Ala	Cys	Ala	Val	Asp	Ala
		35					40				45				
Gly	Ser	Val	Asp	Gln	Thr	Val	Gln	Leu	Gly	Gln	Val	Arg	Thr	Ala	Ser
		50				55					60				
Leu	Ala	Gln	Glu	Gly	Ala	Thr	Ser	Ser	Ala	Val	Gly	Phe	Asn	Ile	Gln
65					70					75				80	
Leu	Asn	Asp	Cys	Asp	Thr	Asn	Val	Ala	Ser	Lys	Ala	Ala	Val	Ala	Phe
			85						90					95	
Leu	Gly	Thr	Ala	Ile	Asp	Ala	Gly	His	Thr	Asn	Val	Leu	Ala	Leu	Gln
			100					105					110		
Ser	Ser	Ala	Ala	Gly	Ser	Ala	Thr	Asn	Val	Gly	Val	Gln	Ile	Leu	Asp
		115					120					125			
Arg	Thr	Gly	Ala	Ala	Leu	Thr	Leu	Asp	Gly	Ala	Thr	Phe	Ser	Ser	Glu
		130				135					140				
Thr	Thr	Leu	Asn	Asn	Gly	Thr	Asn	Thr	Ile	Pro	Phe	Gln	Ala	Arg	Tyr
145					150					155					160
Phe	Ala	Thr	Gly	Ala	Ala	Thr	Pro	Gly	Ala	Ala	Asn	Ala	Asp	Ala	Thr
			165					170						175	
Phe	Lys	Val	Gln	Tyr	Gln										
			180												

<210> 362
 <211> 215
 <212> PRT
 <213> E. Coli

<400> 362

Met	Leu	Leu	Met	Arg	Met	Arg	Pro	Ser	Arg	Phe	Ser	Ile	Asn	Asn	Leu
1			5					10					15		
Pro	Arg	Phe	Arg	Asp	Val	Ile	Thr	Gly	Arg	Asp	Ala	His	Pro	Cys	Ala
			20					25				30			
Ile	Lys	Ile	Thr	Met	Lys	Arg	Lys	Arg	Leu	Phe	Leu	Leu	Ala	Ser	Leu
		35					40					45			
Leu	Pro	Met	Phe	Ala	Leu	Ala	Gly	Asn	Lys	Trp	Asn	Thr	Thr	Leu	Pro
	50					55					60				
Gly	Gly	Asn	Met	Gln	Phe	Gln	Gly	Val	Ile	Ile	Ala	Glu	Thr	Cys	Arg
65				70						75				80	
Ile	Glu	Ala	Gly	Asp	Lys	Gln	Met	Thr	Val	Asn	Met	Gly	Gln	Ile	Ser
				85					90					95	
Ser	Asn	Arg	Phe	His	Ala	Val	Gly	Glu	Asp	Ser	Ala	Pro	Val	Pro	Phe
			100					105					110		
Val	Ile	His	Leu	Arg	Glu	Cys	Ser	Thr	Val	Val	Ser	Glu	Arg	Val	Gly
		115					120					125			
Val	Ala	Phe	His	Gly	Val	Ala	Asp	Gly	Lys	Asn	Pro	Asp	Val	Leu	Ser
	130					135					140				
Val	Gly	Glu	Gly	Pro	Gly	Ile	Ala	Thr	Asn	Ile	Gly	Val	Ala	Leu	Phe
145					150					155				160	
Asp	Asp	Glu	Gly	Asn	Leu	Val	Pro	Ile	Asn	Arg	Pro	Pro	Ala	Asn	Trp
				165					170					175	
Lys	Arg	Leu	Tyr	Ser	Gly	Ser	Thr	Ser	Leu	His	Phe	Ile	Ala	Lys	Tyr
		180						185				190			
Arg	Ala	Thr	Gly	Arg	Arg	Val	Thr	Gly	Gly	Ile	Ala	Asn	Ala	Gln	Ala
		195					200					205			
Trp	Phe	Ser	Leu	Thr	Tyr	Gln									
	210					215									

<210> 363
 <211> 241
 <212> PRT
 <213> E. Coli

<400> 363

Met	Ser	Asn	Lys	Asn	Val	Asn	Val	Arg	Lys	Ser	Gln	Glu	Ile	Thr	Phe
1			5						10					15	
Cys	Leu	Leu	Ala	Gly	Ile	Leu	Met	Phe	Met	Ala	Met	Met	Val	Ala	Gly
			20					25					30		
Arg	Ala	Glu	Ala	Gly	Val	Ala	Leu	Gly	Ala	Thr	Arg	Val	Ile	Tyr	Pro
		35					40					45			
Ala	Gly	Gln	Lys	Gln	Glu	Gln	Leu	Ala	Val	Thr	Asn	Asn	Asp	Glu	Asn
	50					55					60				
Ser	Thr	Tyr	Leu	Ile	Gln	Ser	Trp	Val	Glu	Asn	Ala	Asp	Gly	Val	Lys
65				70						75				80	
Asp	Gly	Arg	Phe	Ile	Val	Thr	Pro	Pro	Leu	Phe	Ala	Met	Lys	Gly	Lys
				85					90					95	

Lys	Glu	Asn	Thr	Leu	Arg	Ile	Leu	Asp	Ala	Thr	Asn	Asn	Gln	Leu	Pro
			100					105					110		
Gln	Asp	Arg	Glu	Ser	Leu	Phe	Trp	Met	Asn	Val	Lys	Ala	Ile	Pro	Ser
		115					120					125			
Met	Asp	Lys	Ser	Lys	Leu	Thr	Glu	Asn	Thr	Leu	Gln	Leu	Ala	Ile	Ile
	130					135					140				
Ser	Arg	Ile	Lys	Leu	Tyr	Tyr	Arg	Pro	Ala	Lys	Leu	Ala	Leu	Pro	Pro
145				150						155					160
Asp	Gln	Ala	Ala	Glu	Lys	Leu	Arg	Phe	Arg	Arg	Ser	Ala	Asn	Ser	Leu
				165					170					175	
Thr	Leu	Ile	Asn	Pro	Thr	Pro	Tyr	Tyr	Leu	Thr	Val	Thr	Glu	Leu	Asn
			180					185					190		
Ala	Gly	Thr	Arg	Val	Leu	Glu	Asn	Ala	Leu	Val	Pro	Pro	Met	Gly	Glu
	195						200					205			
Ser	Thr	Val	Lys	Leu	Pro	Ser	Asp	Ala	Gly	Ser	Asn	Ile	Thr	Tyr	Arg
	210					215					220				
Thr	Ile	Asn	Asp	Tyr	Gly	Ala	Leu	Thr	Pro	Lys	Met	Thr	Gly	Val	Met
225					230					235					240
Glu															

<210> 364
 <211> 878
 <212> PRT
 <213> E. Coli

<400> 364

Met	Ser	Tyr	Leu	Asn	Leu	Arg	Leu	Tyr	Gln	Arg	Asn	Thr	Gln	Cys	Leu
1				5					10					15	
His	Ile	Arg	Lys	His	Arg	Leu	Ala	Gly	Phe	Phe	Val	Arg	Leu	Val	Val
			20					25					30		
Ala	Cys	Ala	Phe	Ala	Ala	Gln	Ala	Pro	Leu	Ser	Ser	Ala	Asp	Leu	Tyr
		35					40					45			
Phe	Asn	Pro	Arg	Phe	Leu	Ala	Asp	Asp	Pro	Gln	Ala	Val	Ala	Asp	Leu
	50					55					60				
Ser	Arg	Phe	Glu	Asn	Gly	Gln	Glu	Leu	Pro	Pro	Gly	Thr	Tyr	Arg	Val
65				70						75				80	
Asp	Ile	Tyr	Leu	Asn	Asn	Gly	Tyr	Met	Ala	Thr	Arg	Asp	Val	Thr	Phe
				85					90					95	
Asn	Thr	Gly	Asp	Ser	Glu	Gln	Gly	Ile	Val	Pro	Cys	Leu	Thr	Arg	Ala
			100					105					110		
Gln	Leu	Ala	Ser	Met	Gly	Leu	Asn	Thr	Ala	Ser	Val	Ala	Gly	Met	Asn
		115					120					125			
Leu	Leu	Ala	Asp	Asp	Ala	Cys	Val	Pro	Leu	Thr	Thr	Met	Val	Gln	Asp
	130					135						140			
Ala	Thr	Ala	His	Leu	Asp	Val	Gly	Gln	Gln	Arg	Leu	Asn	Leu	Thr	Ile
145				150						155					160
Pro	Gln	Ala	Phe	Met	Ser	Asn	Arg	Ala	Arg	Gly	Tyr	Ile	Pro	Pro	Glu
				165					170					175	
Leu	Trp	Asp	Pro	Gly	Ile	Asn	Ala	Gly	Leu	Leu	Asn	Tyr	Asn	Phe	Ser
			180					185					190		
Gly	Asn	Ser	Val	Gln	Asn	Arg	Ile	Gly	Gly	Asn	Ser	His	Tyr	Ala	Tyr
		195					200					205			
Leu	Asn	Leu	Gln	Ser	Gly	Leu	Asn	Ile	Gly	Ala	Trp	Arg	Leu	Arg	Asp
	210					215					220				
Asn	Thr	Thr	Trp	Ser	Tyr	Asn	Ser	Ser	Asp	Arg	Ser	Ser	Gly	Ser	Lys

225					230					235					240
Asn	Lys	Trp	Gln	His	Ile	Asn	Thr	Trp	Leu	Glu	Arg	Asp	Ile	Ile	Pro
				245					250					255	
Leu	Arg	Ser	Arg	Leu	Thr	Leu	Gly	Asp	Gly	Tyr	Thr	Gln	Gly	Asp	Ile
			260					265					270		
Phe	Asp	Gly	Ile	Asn	Phe	Arg	Gly	Ala	Gln	Leu	Ala	Ser	Asp	Asp	Asn
		275					280					285			
Met	Leu	Pro	Asp	Ser	Gln	Arg	Gly	Phe	Ala	Pro	Val	Ile	His	Gly	Ile
	290					295					300				
Ala	Arg	Gly	Thr	Ala	Gln	Val	Thr	Ile	Lys	Gln	Asn	Gly	Tyr	Asp	Ile
305					310					315					320
Tyr	Asn	Ser	Thr	Val	Pro	Pro	Gly	Pro	Phe	Thr	Ile	Asn	Asp	Ile	Tyr
				325					330					335	
Ala	Ala	Gly	Asn	Ser	Gly	Asp	Leu	Gln	Val	Thr	Ile	Lys	Glu	Ala	Asp
			340					345					350		
Gly	Ser	Thr	Gln	Ile	Phe	Thr	Val	Pro	Tyr	Ser	Ser	Val	Pro	Leu	Leu
		355					360					365			
Gln	Arg	Glu	Gly	His	Thr	Arg	Tyr	Ser	Ile	Thr	Ala	Gly	Glu	Tyr	Arg
	370					375					380				
Ser	Gly	Asn	Ala	Gln	Gln	Glu	Lys	Thr	Arg	Phe	Phe	Gln	Ser	Thr	Leu
385					390					395					400
Leu	His	Gly	Leu	Pro	Ala	Gly	Trp	Thr	Ile	Tyr	Gly	Gly	Thr	Gln	Leu
				405					410					415	
Ala	Asp	Arg	Tyr	Arg	Ala	Phe	Asn	Phe	Gly	Ile	Gly	Lys	Asn	Met	Gly
			420					425					430		
Ala	Leu	Gly	Ala	Leu	Ser	Val	Asp	Met	Thr	Gln	Ala	Asn	Ser	Thr	Leu
		435					440					445			
Pro	Asp	Asp	Ser	Gln	His	Asp	Gly	Gln	Ser	Val	Arg	Phe	Leu	Tyr	Asn
	450					455					460				
Lys	Ser	Leu	Asn	Glu	Ser	Gly	Thr	Asn	Ile	Gln	Leu	Val	Gly	Tyr	Arg
465					470					475					480
Tyr	Ser	Thr	Ser	Gly	Tyr	Phe	Asn	Phe	Ala	Asp	Thr	Thr	Tyr	Ser	Arg
			485						490					495	
Met	Asn	Gly	Tyr	Asn	Ile	Glu	Thr	Gln	Asp	Gly	Val	Ile	Gln	Val	Lys
		500						505					510		
Pro	Lys	Phe	Thr	Asp	Tyr	Tyr	Asn	Leu	Ala	Tyr	Asn	Lys	Arg	Gly	Lys
		515					520					525			
Leu	Gln	Leu	Thr	Val	Thr	Gln	Gln	Leu	Gly	Arg	Thr	Ser	Thr	Leu	Tyr
	530					535					540				
Leu	Ser	Gly	Ser	His	Gln	Thr	Tyr	Trp	Gly	Thr	Ser	Asn	Val	Asp	Glu
545					550					555					560
Gln	Phe	Gln	Ala	Gly	Leu	Asn	Thr	Ala	Phe	Glu	Asp	Ile	Asn	Trp	Thr
				565					570					575	
Leu	Ser	Tyr	Ser	Leu	Thr	Lys	Asn	Ala	Trp	Gln	Lys	Gly	Arg	Asp	Gln
			580					585					590		
Met	Leu	Ala	Leu	Asn	Val	Asn	Ile	Pro	Phe	Ser	His	Trp	Leu	Arg	Ser
		595					600					605			
Asp	Ser	Lys	Ser	Gln	Trp	Arg	His	Ala	Ser	Ala	Ser	Tyr	Ser	Met	Ser
	610					615						620			
His	Asp	Leu	Asn	Gly	Arg	Met	Thr	Asn	Leu	Ala	Gly	Val	Tyr	Gly	Thr
625					630					635					640
Leu	Leu	Glu	Asp	Asn	Asn	Leu	Ser	Tyr	Ser	Val	Gln	Thr	Gly	Tyr	Ala
				645					650					655	
Gly	Gly	Gly	Asp	Gly	Asn	Ser	Gly	Ser	Thr	Gly	Tyr	Ala	Thr	Leu	Asn
			660				665						670		
Tyr	Arg	Gly	Gly	Tyr	Gly	Asn	Ala	Asn	Ile	Gly	Tyr	Ser	His	Ser	Asp
		675					680					685			

Asp	Ile	Lys	Gln	Leu	Tyr	Tyr	Gly	Val	Ser	Gly	Gly	Val	Leu	Ala	His
690						695				700					
Ala	Asn	Gly	Val	Thr	Leu	Gly	Gln	Pro	Leu	Asn	Asp	Thr	Val	Val	Leu
705					710					715					720
Val	Lys	Ala	Pro	Gly	Ala	Lys	Asp	Ala	Lys	Val	Glu	Asn	Gln	Thr	Gly
				725					730						735
Val	Arg	Thr	Asp	Trp	Arg	Gly	Tyr	Ala	Val	Leu	Pro	Tyr	Ala	Thr	Glu
			740					745					750		
Tyr	Arg	Glu	Asn	Arg	Val	Ala	Leu	Asp	Thr	Asn	Thr	Leu	Ala	Asp	Asn
		755					760					765			
Val	Asp	Leu	Asp	Asn	Ala	Val	Ala	Asn	Val	Val	Pro	Thr	Arg	Gly	Ala
	770					775					780				
Ile	Val	Arg	Ala	Glu	Phe	Lys	Ala	Arg	Val	Gly	Ile	Lys	Leu	Leu	Met
785					790					795					800
Thr	Leu	Thr	His	Asn	Asn	Lys	Pro	Leu	Pro	Phe	Gly	Ala	Met	Val	Thr
				805					810					815	
Ser	Glu	Ser	Ser	Gln	Ser	Ser	Gly	Ile	Val	Ala	Asp	Asn	Gly	Gln	Val
			820					825					830		
Tyr	Leu	Ser	Gly	Met	Pro	Leu	Ala	Gly	Lys	Val	Gln	Val	Lys	Trp	Gly
		835					840					845			
Glu	Glu	Glu	Asn	Ala	His	Cys	Val	Ala	Asn	Tyr	Gln	Leu	Pro	Pro	Glu
	850					855					860				
Ser	Gln	Gln	Gln	Leu	Leu	Thr	Gln	Leu	Ser	Ala	Glu	Cys	Arg		
865					870					875					

<210> 365
 <211> 176
 <212> PRT
 <213> E. Coli

<400> 365															
Met	Arg	Asn	Lys	Pro	Phe	Tyr	Leu	Leu	Cys	Ala	Phe	Leu	Trp	Leu	Ala
1				5					10					15	
Val	Ser	His	Ala	Leu	Ala	Ala	Asp	Ser	Thr	Ile	Thr	Ile	Arg	Gly	Tyr
			20					25					30		
Val	Arg	Asp	Asn	Gly	Cys	Ser	Val	Ala	Ala	Glu	Ser	Thr	Asn	Phe	Thr
		35					40					45			
Val	Asp	Leu	Met	Glu	Asn	Ala	Ala	Lys	Gln	Phe	Asn	Asn	Ile	Gly	Ala
	50					55					60				
Thr	Thr	Pro	Val	Val	Pro	Phe	Arg	Ile	Leu	Leu	Ser	Pro	Cys	Gly	Asn
65					70					75					80
Ala	Val	Ser	Ala	Val	Lys	Val	Gly	Phe	Thr	Gly	Val	Ala	Asp	Ser	His
				85					90					95	
Asn	Ala	Asn	Leu	Leu	Ala	Leu	Glu	Asn	Thr	Val	Ser	Ala	Ala	Ser	Gly
			100					105					110		
Leu	Gly	Ile	Gln	Leu	Leu	Asn	Glu	Gln	Gln	Asn	Gln	Ile	Pro	Leu	Asn
		115					120					125			
Ala	Pro	Ser	Ser	Ala	Leu	Ser	Trp	Thr	Thr	Leu	Thr	Pro	Gly	Lys	Pro
	130					135					140				
Asn	Thr	Leu	Asn	Phe	Tyr	Ala	Arg	Leu	Met	Ala	Thr	Gln	Val	Pro	Val
145					150					155					160
Thr	Ala	Gly	His	Ile	Asn	Ala	Thr	Ala	Thr	Phe	Thr	Leu	Glu	Tyr	Gln
				165					170					175	

<210> 366
 <211> 167
 <212> PRT
 <213> E. Coli

<400> 366

Met	Lys	Trp	Cys	Lys	Arg	Gly	Tyr	Val	Leu	Ala	Ala	Ile	Leu	Ala	Leu
1				5					10					15	
Ala	Ser	Ala	Thr	Ile	Gln	Ala	Ala	Asp	Val	Thr	Ile	Thr	Val	Asn	Gly
			20					25					30		
Lys	Val	Val	Ala	Lys	Pro	Cys	Thr	Val	Ser	Thr	Thr	Asn	Ala	Thr	Val
		35					40					45			
Asp	Leu	Gly	Asp	Leu	Tyr	Ser	Phe	Ser	Leu	Met	Ser	Ala	Gly	Ala	Ala
	50					55					60				
Ser	Ala	Trp	His	Asp	Val	Ala	Leu	Glu	Leu	Thr	Asn	Cys	Pro	Val	Gly
65					70					75					80
Thr	Ser	Arg	Val	Thr	Ala	Ser	Phe	Ser	Gly	Ala	Ala	Asp	Ser	Thr	Gly
				85					90					95	
Tyr	Tyr	Lys	Asn	Gln	Gly	Thr	Ala	Gln	Asn	Ile	Gln	Leu	Glu	Leu	Gln
			100					105					110		
Asp	Asp	Ser	Gly	Asn	Thr	Leu	Asn	Thr	Gly	Ala	Thr	Lys	Thr	Val	Gln
		115					120					125			
Val	Asp	Asp	Ser	Ser	Gln	Ser	Ala	His	Phe	Pro	Leu	Gln	Val	Arg	Ala
	130					135					140				
Leu	Thr	Val	Asn	Gly	Gly	Ala	Thr	Gln	Gly	Thr	Ile	Gln	Ala	Val	Ile
145					150					155					160
Ser	Ile	Thr	Tyr	Thr	Tyr	Ser									
				165											

<210> 367
 <211> 300
 <212> PRT
 <213> E. Coli

<400> 367

Met	Lys	Arg	Val	Ile	Thr	Leu	Phe	Ala	Val	Leu	Leu	Met	Gly	Trp	Ser
1				5					10					15	
Val	Asn	Ala	Trp	Ser	Phe	Ala	Cys	Lys	Thr	Ala	Asn	Gly	Thr	Ala	Ile
			20					25					30		
Pro	Ile	Gly	Gly	Gly	Ser	Ala	Asn	Val	Tyr	Val	Asn	Leu	Ala	Pro	Val
		35					40					45			
Val	Asn	Val	Gly	Gln	Asn	Leu	Val	Val	Asp	Leu	Ser	Thr	Gln	Ile	Phe
	50					55					60				
Cys	His	Asn	Asp	Tyr	Pro	Glu	Thr	Ile	Thr	Asp	Tyr	Val	Thr	Leu	Gln
65					70					75					80
Arg	Gly	Ser	Ala	Tyr	Gly	Gly	Val	Leu	Ser	Asn	Phe	Ser	Gly	Thr	Val
				85					90					95	
Lys	Tyr	Ser	Gly	Ser	Ser	Tyr	Pro	Phe	Pro	Thr	Thr	Ser	Glu	Thr	Pro
			100					105					110		
Arg	Val	Val	Tyr	Asn	Ser	Arg	Thr	Asp	Lys	Pro	Trp	Pro	Val	Ala	Leu
		115					120					125			
Tyr	Leu	Thr	Pro	Val	Ser	Ser	Ala	Gly	Gly	Val	Ala	Ile	Lys	Ala	Gly
	130					135					140				
Ser	Leu	Ile	Ala	Val	Leu	Ile	Leu	Arg	Gln	Thr	Asn	Asn	Tyr	Asn	Ser
145					150					155					160

Asp	Asp	Phe	Gln	Phe	Val	Trp	Asn	Ile	Tyr	Ala	Asn	Asn	Asp	Val	Val
				165					170					175	
Val	Pro	Thr	Gly	Gly	Cys	Asp	Val	Ser	Ala	Arg	Asp	Val	Thr	Val	Thr
			180					185					190		
Leu	Pro	Asp	Tyr	Pro	Gly	Ser	Val	Pro	Ile	Pro	Leu	Thr	Val	Tyr	Cys
		195					200					205			
Ala	Lys	Ser	Gln	Asn	Leu	Gly	Tyr	Tyr	Leu	Ser	Gly	Thr	Thr	Ala	Asp
	210					215					220				
Ala	Gly	Asn	Ser	Ile	Phe	Thr	Asn	Thr	Ala	Ser	Phe	Ser	Pro	Ala	Gln
225					230					235					240
Gly	Val	Gly	Val	Gln	Leu	Thr	Arg	Asn	Gly	Thr	Ile	Ile	Pro	Ala	Asn
				245					250					255	
Asn	Thr	Val	Ser	Leu	Gly	Ala	Val	Gly	Thr	Ser	Ala	Val	Ser	Leu	Gly
			260					265					270		
Leu	Thr	Ala	Asn	Tyr	Ala	Arg	Thr	Gly	Gly	Gln	Val	Thr	Ala	Gly	Asn
		275					280					285			
Val	Gln	Ser	Ile	Ile	Gly	Val	Thr	Phe	Val	Tyr	Gln				
	290					295					300				

<210> 368
 <211> 521
 <212> PRT
 <213> E. Coli

<400> 368															
Met	Leu	Ser	Lys	Leu	Pro	Arg	Arg	Leu	Arg	Ser	Phe	Gln	Thr	Tyr	Cys
1				5					10					15	
Thr	Ile	Arg	Val	His	Arg	Gly	Glu	Asp	Met	Lys	Ser	Met	Asp	Lys	Leu
			20					25					30		
Thr	Thr	Gly	Val	Ala	Tyr	Gly	Thr	Ser	Ala	Gly	Asn	Ala	Gly	Phe	Trp
		35					40					45			
Ala	Leu	Gln	Leu	Leu	Asp	Lys	Val	Thr	Pro	Ser	Gln	Trp	Ala	Ala	Ile
	50					55					60				
Gly	Val	Leu	Gly	Ser	Leu	Val	Phe	Gly	Leu	Leu	Thr	Tyr	Leu	Thr	Asn
65					70				75						80
Leu	Tyr	Phe	Lys	Ile	Lys	Glu	Asp	Arg	Arg	Lys	Ala	Ala	Arg	Gly	Glu
				85				90						95	
Ser	Asn	Asp	Ser	Arg	Leu	Thr	Gly	Cys	Glu	Arg	Ser	Pro	Phe	Glu	Ser
			100					105					110		
Tyr	Gly	Asn	Cys	Ser	Leu	Thr	Gly	Gln	Arg	Thr	Leu	Arg	Asn	Phe	Pro
		115					120					125			
Gly	Cys	Arg	His	Gly	Pro	Cys	Arg	Ser	Cys	Ala	Gly	Val	Leu	Gly	Ser
	130					135					140				
Ser	Gln	Lys	Glu	Arg	Pro	Ala	Ser	Leu	Pro	Gly	Ser	Ser	Arg	Lys	Ile
145					150					155					160
Val	Arg	Lys	Ser	Val	Leu	Ser	Ala	Ala	Ser	Val	Leu	Leu	Asp	Lys	Ser
				165					170					175	
Cys	Gln	Ala	Arg	Ala	Ser	Ser	Ser	Ile	Ser	Met	Asn	Thr	Lys	Ile	Arg
			180					185					190		
Tyr	Gly	Leu	Ser	Ala	Ala	Val	Leu	Ala	Leu	Ile	Gly	Ala	Gly	Ala	Ser
		195					200					205			
Ala	Pro	Gln	Ile	Leu	Asp	Gln	Phe	Leu	Asp	Glu	Lys	Glu	Gly	Asn	His
	210					215					220				
Thr	Met	Ala	Tyr	Arg	Asp	Gly	Ser	Gly	Ile	Trp	Thr	Ile	Cys	Arg	Gly
225					230					235					240

Ala	Thr	Val	Val	Asp	Gly	Lys	Thr	Val	Phe	Pro	Asn	Met	Lys	Leu	Ser		
				245					250					255			
Lys	Glu	Lys	Cys	Asp	Gln	Val	Asn	Ala	Ile	Glu	Arg	Asp	Lys	Ala	Leu		
			260					265					270				
Ala	Trp	Val	Glu	Arg	Asn	Ile	Lys	Val	Pro	Leu	Thr	Glu	Pro	Gln	Lys		
		275					280					285					
Ala	Gly	Ile	Ala	Ser	Phe	Cys	Pro	Tyr	Asn	Ile	Gly	Pro	Gly	Lys	Cys		
	290					295					300						
Phe	Pro	Ser	Thr	Phe	Tyr	Lys	Arg	Leu	Asn	Ala	Gly	Asp	Arg	Lys	Gly		
305					310					315					320		
Ala	Cys	Glu	Ala	Ile	Arg	Trp	Trp	Ile	Lys	Asp	Gly	Gly	Arg	Asp	Cys		
				325					330					335			
Arg	Ile	Arg	Ser	Asn	Asn	Cys	Tyr	Gly	Gln	Val	Ile	Arg	Arg	Asp	Gln		
			340					345						350			
Glu	Ser	Ala	Leu	Thr	Cys	Trp	Gly	Ile	Glu	Gln	Ile	Arg	Tyr	Ser	Trp		
		355					360					365					
Phe	Phe	Ser	Cys	Cys	Gln	Asp	Leu	Ser	Ser	Glu	Met	Ser	Gly	Ala	Thr		
	370					375					380						
Glu	Asp	Gly	Lys	Lys	Asn	Gly	Arg	Asn	Val	Met	Leu	Pro	His	Tyr	His		
385					390					395					400		
Lys	Arg	Met	Leu	Asn	Leu	Leu	Leu	Glu	Leu	Asn	Arg	Gly	Glu	Leu	Pro		
				405					410					415			
Val	Met	Arg	Leu	Leu	Lys	Met	Arg	Asn	Arg	Asn	Leu	Leu	Lys	Phe	Leu		
			420					425					430				
Pro	Gly	Leu	Leu	Ile	Cys	Leu	Ile	Val	Leu	Thr	Ser	Cys	Val	Pro	Lys		
		435				440						445					
Gln	Lys	Asn	Met	Pro	Tyr	Ala	Leu	Thr	Gln	Arg	Ser	Ile	Pro	Gln	Ile		
	450					455					460						
Leu	Pro	Leu	Pro	Ser	Glu	Ala	Lys	Gln	Pro	Lys	Pro	Pro	Lys	Glu	Cys		
465					470					475					480		
Ser	Pro	Thr	Cys	Ser	Glu	Ile	Leu	Gln	Gln	Lys	Leu	Ser	Phe	Met	Leu		
				485					490					495			
Lys	Leu	Leu	Thr	Asn	Ala	Thr	Ser	Gln	Glu	Leu	Val	Asn	Arg	Ser	Met		
			500					505					510				
Asn	Leu	Glu	Ile	Lys	Ser	Ile	Lys	Cys									
		515					520										

<210> 369

<211> 177

<212> PRT

<213> E. Coli

<400> 369

Met	Asn	Thr	Lys	Ile	Arg	Tyr	Gly	Leu	Ser	Ala	Ala	Val	Leu	Ala	Leu		
1				5				10					15				
Ile	Gly	Ala	Gly	Ala	Ser	Ala	Pro	Gln	Ile	Leu	Asp	Gln	Phe	Leu	Asp		
		20						25				30					
Glu	Lys	Glu	Gly	Asn	His	Thr	Met	Ala	Tyr	Arg	Asp	Gly	Ser	Gly	Ile		
	35					40					45						
Trp	Thr	Ile	Cys	Arg	Gly	Ala	Thr	Val	Val	Asp	Gly	Lys	Thr	Val	Phe		
	50					55				60							
Pro	Asn	Met	Lys	Leu	Ser	Lys	Glu	Lys	Cys	Asp	Gln	Val	Asn	Ala	Ile		
65					70				75						80		
Glu	Arg	Asp	Lys	Ala	Leu	Ala	Trp	Val	Glu	Arg	Asn	Ile	Lys	Val	Pro		
				85				90						95			

Leu	Thr	Glu	Pro	Gln	Lys	Ala	Gly	Ile	Ala	Ser	Phe	Cys	Pro	Tyr	Asn
			100					105					110		
Ile	Gly	Pro	Gly	Lys	Cys	Phe	Pro	Ser	Thr	Phe	Tyr	Lys	Arg	Leu	Asn
		115					120					125			
Ala	Gly	Asp	Arg	Lys	Gly	Ala	Cys	Glu	Ala	Ile	Arg	Trp	Trp	Ile	Lys
		130				135					140				
Asp	Gly	Gly	Arg	Asp	Cys	Arg	Ile	Arg	Ser	Asn	Asn	Cys	Tyr	Gly	Gln
145					150					155					160
Val	Ile	Arg	Arg	Asp	Gln	Glu	Ser	Ala	Leu	Thr	Cys	Trp	Gly	Ile	Glu
				165					170					175	

Gln

<210> 370
 <211> 103
 <212> PRT
 <213> E. Coli

<400> 370

Met	Thr	Gln	Asp	Tyr	Glu	Leu	Val	Val	Lys	Gly	Val	Arg	Asn	Phe	Glu
1				5					10					15	
Asn	Lys	Val	Thr	Val	Thr	Val	Ala	Leu	Gln	Asp	Lys	Glu	Arg	Phe	Asp
			20					25					30		
Gly	Glu	Ile	Phe	Asp	Leu	Asp	Val	Ala	Met	Asp	Arg	Val	Glu	Gly	Ala
		35				40						45			
Ala	Leu	Glu	Phe	Tyr	Glu	Ala	Ala	Ala	Arg	Arg	Ser	Val	Arg	Gln	Val
	50					55					60				
Phe	Leu	Glu	Val	Ala	Glu	Lys	Leu	Ser	Glu	Lys	Val	Glu	Ser	Tyr	Leu
65					70					75					80
Gln	His	Gln	Tyr	Ser	Phe	Lys	Ile	Glu	Asn	Pro	Ala	Asn	Lys	His	Glu
				85					90					95	

Arg Pro His His Lys Tyr Leu
 100

<210> 371
 <211> 96
 <212> PRT
 <213> E. Coli

<400> 371

Met	Leu	Ser	Lys	Leu	Pro	Arg	Arg	Leu	Arg	Ser	Phe	Gln	Thr	Tyr	Cys
1				5					10					15	
Thr	Ile	Arg	Val	His	Arg	Gly	Glu	Asp	Met	Lys	Ser	Met	Asp	Lys	Leu
			20					25					30		
Thr	Thr	Gly	Val	Ala	Tyr	Gly	Thr	Ser	Ala	Gly	Asn	Ala	Gly	Phe	Trp
		35					40					45			
Ala	Leu	Gln	Leu	Leu	Asp	Lys	Val	Thr	Pro	Ser	Gln	Trp	Ala	Ala	Ile
	50					55					60				
Gly	Val	Leu	Gly	Ser	Leu	Val	Phe	Gly	Leu	Leu	Thr	Tyr	Leu	Thr	Asn
65					70					75					80
Leu	Tyr	Phe	Lys	Ile	Lys	Glu	Asp	Arg	Arg	Lys	Ala	Ala	Arg	Gly	Glu
				85					90					95	

<210> 372
 <211> 71
 <212> PRT
 <213> E. Coli

<400> 372
 Met Ser Asn Lys Met Thr Gly Leu Val Lys Trp Phe Asn Ala Asp Lys
 1 5 10 15
 Gly Phe Gly Phe Ile Ser Pro Val Asp Gly Ser Lys Asp Val Phe Val
 20 25 30
 His Phe Ser Ala Ile Gln Asn Asp Tyr Arg Thr Leu Phe Glu Gly
 35 40 45
 Gln Lys Val Thr Phe Ser Ile Glu Ser Gly Ala Lys Gly Pro Ala Ala
 50 55 60
 Ala Asn Val Ile Ile Thr Asp
 65 70

<210> 373
 <211> 338
 <212> PRT
 <213> E. Coli

<400> 373
 Met Phe Val Ile Trp Ser His Arg Thr Gly Phe Ile Met Ser His Gln
 1 5 10 15
 Leu Thr Phe Ala Asp Ser Glu Phe Ser Ser Lys Arg Arg Gln Thr Arg
 20 25 30
 Lys Glu Ile Phe Leu Ser Arg Met Glu Gln Ile Leu Pro Trp Gln Asn
 35 40 45
 Met Val Glu Val Ile Glu Pro Phe Tyr Pro Lys Ala Gly Asn Gly Arg
 50 55 60
 Arg Pro Tyr Pro Leu Glu Thr Met Leu Arg Ile His Cys Met Gln His
 65 70 75 80
 Trp Tyr Asn Leu Ser Asp Gly Ala Met Glu Asp Ala Leu Tyr Glu Ile
 85 90 95
 Ala Ser Met Arg Leu Phe Ala Arg Leu Ser Leu Asp Ser Ala Leu Pro
 100 105 110
 Asp Arg Thr Thr Ile Met Asn Phe Arg His Leu Leu Glu Gln His Gln
 115 120 125
 Leu Ala Arg Gln Leu Phe Lys Thr Ile Asn Arg Trp Leu Ala Glu Ala
 130 135 140
 Gly Val Met Met Thr Gln Gly Thr Leu Val Asp Ala Thr Ile Ile Glu
 145 150 155 160
 Ala Pro Ser Ser Thr Lys Asn Lys Glu Gln Gln Arg Asp Pro Glu Met
 165 170 175
 His Gln Thr Lys Lys Gly Asn Gln Trp His Phe Gly Met Lys Ala His
 180 185 190
 Ile Gly Val Asp Ala Lys Ser Gly Leu Thr His Ser Leu Val Thr Thr
 195 200 205
 Ala Ala Asn Glu His Asp Leu Asn Gln Leu Gly Asn Leu Leu His Gly
 210 215 220
 Glu Glu Gln Phe Val Ser Ala Asp Ala Gly Tyr Gln Gly Ala Pro Gln
 225 230 235 240
 Arg Glu Glu Leu Ala Glu Val Asp Val Asp Trp Leu Ile Ala Glu Arg

Pro	Gly	Lys	Val	Arg	Thr	Leu	Lys	Gln	His	Pro	Arg	Lys	Asn	Lys	Thr
			260					265					270		
Ala	Ile	Asn	Ile	Glu	Tyr	Met	Lys	Ala	Ser	Ile	Arg	Ala	Arg	Val	Glu
		275					280					285			
His	Pro	Phe	Arg	Ile	Ile	Lys	Arg	Gln	Phe	Gly	Phe	Val	Lys	Ala	Arg
	290					295				300					
Tyr	Lys	Gly	Leu	Leu	Lys	Asn	Asp	Asn	Gln	Leu	Ala	Met	Leu	Phe	Thr
305					310				315						320
Leu	Ala	Asn	Leu	Phe	Arg	Ala	Asp	Gln	Met	Ile	Arg	Gln	Trp	Glu	Arg
			325					330					335		
Ser	His														

<210> 374
 <211> 157
 <212> PRT
 <213> E. Coli

<400> 374

Met	Val	Tyr	Ile	Ile	Ile	Val	Ser	His	Gly	His	Glu	Asp	Tyr	Ile	Lys
1				5					10					15	
Lys	Leu	Leu	Glu	Asn	Leu	Asn	Ala	Asp	Asp	Glu	His	Tyr	Lys	Ile	Ile
			20					25					30		
Val	Arg	Asp	Asn	Lys	Asp	Ser	Leu	Leu	Leu	Lys	Gln	Ile	Cys	Gln	His
		35				40						45			
Tyr	Ala	Gly	Leu	Asp	Tyr	Ile	Ser	Gly	Gly	Val	Tyr	Gly	Phe	Gly	His
	50					55				60					
Asn	Asn	Asn	Ile	Ala	Val	Ala	Tyr	Val	Lys	Glu	Lys	Tyr	Arg	Pro	Ala
65					70					75					80
Asp	Asp	Asp	Tyr	Ile	Leu	Phe	Leu	Asn	Pro	Asp	Ile	Ile	Met	Lys	His
				85				90						95	
Asp	Asp	Leu	Leu	Thr	Tyr	Ile	Lys	Tyr	Val	Glu	Ser	Lys	Arg	Tyr	Ala
			100					105					110		
Phe	Ser	Thr	Leu	Cys	Leu	Phe	Arg	Asp	Glu	Ala	Lys	Ser	Leu	His	Asp
		115					120					125			
Tyr	Ser	Val	Arg	Lys	Phe	Pro	Val	Leu	Ser	Asp	Phe	Ile	Val	Ser	Phe
	130					135					140				
Met	Leu	Gly	Ile	Lys	Glu	Gly	Ala	Asn	Lys	Ser	Leu	Ile			
145					150					155					

<210> 375
 <211> 372
 <212> PRT
 <213> E. Coli

<400> 375

Met	Gly	Lys	Ser	Ile	Val	Val	Val	Ser	Ala	Val	Asn	Phe	Thr	Thr	Gly
1				5					10					15	
Gly	Pro	Phe	Thr	Ile	Leu	Lys	Lys	Phe	Leu	Ala	Ala	Thr	Asn	Asn	Lys
			20					25					30		
Glu	Asn	Val	Ser	Phe	Ile	Ala	Leu	Val	His	Ser	Ala	Lys	Glu	Leu	Lys
		35					40					45			
Glu	Ser	Tyr	Pro	Trp	Val	Lys	Phe	Ile	Glu	Phe	Pro	Glu	Val	Lys	Gly

50		55		60
Ser Trp Leu Lys Arg	Leu His Phe Glu Tyr Val	Val Cys Lys Lys Leu		
65	70	75	80	
Ser Lys Glu Leu Asn	Ala Thr His Trp Ile Cys	Leu His Asp Ile Thr		
	85	90	95	
Ala Asn Val Val Thr	Lys Lys Arg Tyr Val Tyr	Cys His Asn Pro Ala		
	100	105	110	
Pro Phe Tyr Lys Gly	Ile Leu Phe Arg Glu Ile	Leu Met Glu Pro Ser		
	115	120	125	
Phe Phe Leu Phe Lys	Met Leu Tyr Gly Leu Ile	Tyr Lys Ile Asn Ile		
	130	135	140	
Lys Lys Asn Thr Ala	Val Phe Val Gln Gln	Phe Trp Met Lys Glu Lys		
145	150	155	160	
Phe Ile Lys Lys Tyr	Ser Ile Asn Asn Ile	Ile Val Ser Arg Pro Glu		
	165	170	175	
Ile Lys Leu Ser Asp	Lys Ser Gln Leu Thr	Asp Asp Asp Ser Gln Phe		
	180	185	190	
Lys Asn Asn Pro Ser	Glu Leu Thr Ile Phe Tyr	Pro Ala Val Pro Arg		
	195	200	205	
Val Phe Lys Asn Tyr	Glu Leu Ile Ile Ser	Ala Ala Arg Lys Leu Lys		
	210	215	220	
Glu Gln Ser Asn Ile	Lys Phe Leu Leu Thr	Ile Ser Gly Thr Glu Asn		
225	230	235	240	
Ala Tyr Ala Lys Tyr	Ile Ile Ser Leu Ala	Glu Gly Leu Asp Asn Val		
	245	250	255	
His Phe Leu Gly Tyr	Leu Asp Lys Glu Lys	Ile Asp His Cys Tyr Asn		
	260	265	270	
Ile Ser Asp Ile Val	Cys Phe Pro Ser Arg	Leu Glu Thr Trp Gly Leu		
	275	280	285	
Pro Leu Ser Glu Ala	Lys Glu Arg Gly Lys	Trp Val Leu Ala Ser Asp		
	290	295	300	
Phe Pro Phe Thr Arg	Glu Thr Leu Gly Ser	Tyr Glu Lys Lys Ala Phe		
305	310	315	320	
Phe Asp Ser Asn Asn	Asp Asp Met Leu Val	Lys Leu Ile Ile Asp Phe		
	325	330	335	
Lys Lys Gly Asn Leu	Lys Lys Asp Ile Ser	Asp Ala Asn Phe Ile Tyr		
	340	345	350	
Arg Asn Glu Asn Val	Leu Val Gly Phe Asp	Glu Leu Val Asn Phe Ile		
	355	360	365	
Thr Glu Glu His				
370				

<210> 376
 <211> 196
 <212> PRT
 <213> E. Coli

<400>	376
Met Ile Leu Lys Leu	Ala Lys Arg Tyr Gly
1	5
Leu Val Arg Asp Val	Leu Leu Thr Arg
	20
Ile Ile Arg Phe Pro	Cys Tyr Ile Arg
	35
Gly Glu Asn Phe Thr	Ser Gly Val Gly
50	55

Arg	Gly	Val	Ile	Phe	Phe	Ser	Asp	Asn	Val	Gln	Val	Asn	Asp	Tyr	Val
65					70					75					80
His	Ile	Ala	Ser	Ile	Glu	Ser	Val	Thr	Ile	Gly	Arg	Asp	Thr	Leu	Ile
				85					90					95	
Ala	Ser	Lys	Val	Phe	Ile	Thr	Asp	His	Asn	His	Gly	Ser	Phe	Lys	His
			100					105					110		
Ser	Asp	Pro	Met	Ser	Ser	Pro	Asn	Ile	Pro	Pro	Asp	Met	Arg	Thr	Leu
		115					120					125			
Glu	Ser	Ser	Ala	Val	Val	Ile	Gly	Gln	Arg	Val	Trp	Leu	Gly	Glu	Asn
	130					135					140				
Val	Thr	Val	Leu	Pro	Gly	Thr	Ile	Ile	Gly	Asn	Gly	Val	Val	Val	Gly
145					150					155					160
Ala	Asn	Ser	Val	Val	Arg	Gly	Ser	Ile	Pro	Glu	Asn	Thr	Val	Ile	Ala
			165						170					175	
Gly	Val	Pro	Ala	Lys	Ile	Ile	Lys	Lys	Tyr	Asn	His	Glu	Thr	Lys	Leu
			180					185						190	
Trp	Glu	Lys	Ala												
			195												

<210> 377

<211> 330

<212> PRT

<213> E. Coli

<400> 377

Met	Tyr	Phe	Leu	Asn	Asp	Leu	Asn	Phe	Ser	Arg	Arg	Asp	Ala	Gly	Phe
1				5				10						15	
Lys	Ala	Arg	Lys	Asp	Ala	Leu	Asp	Ile	Ala	Ser	Asp	Tyr	Glu	Asn	Ile
			20					25					30		
Ser	Val	Val	Asn	Ile	Pro	Leu	Trp	Gly	Gly	Val	Val	Gln	Arg	Ile	Ile
			35				40					45			
Ser	Ser	Val	Lys	Leu	Ser	Thr	Phe	Leu	Cys	Gly	Leu	Glu	Asn	Lys	Asp
			50			55					60				
Val	Leu	Ile	Phe	Asn	Phe	Pro	Met	Ala	Lys	Pro	Phe	Trp	His	Ile	Leu
65					70					75					80
Ser	Phe	Phe	His	Arg	Leu	Leu	Lys	Phe	Arg	Ile	Val	Pro	Leu	Ile	His
			85					90						95	
Asp	Ile	Asp	Glu	Leu	Arg	Gly	Gly	Gly	Gly	Ser	Asp	Ser	Val	Arg	Leu
			100					105					110		
Ala	Thr	Cys	Asp	Met	Val	Ile	Ser	His	Asn	Pro	Gln	Met	Thr	Lys	Tyr
			115				120					125			
Leu	Ser	Lys	Tyr	Met	Ser	Gln	Asp	Lys	Ile	Lys	Asp	Ile	Lys	Ile	Phe
			130			135					140				
Asp	Tyr	Leu	Val	Ser	Ser	Asp	Val	Glu	His	Arg	Asp	Val	Thr	Asp	Lys
145					150					155					160
Gln	Arg	Gly	Val	Ile	Tyr	Ala	Gly	Asn	Leu	Ser	Arg	His	Lys	Cys	Ser
			165					170						175	
Phe	Ile	Tyr	Thr	Glu	Gly	Cys	Asp	Phe	Thr	Leu	Phe	Gly	Val	Asn	Tyr
			180					185					190		
Glu	Asn	Lys	Asp	Asn	Pro	Lys	Tyr	Leu	Gly	Ser	Phe	Asp	Ala	Gln	Ser
		195					200					205			
Pro	Glu	Lys	Ile	Asn	Leu	Pro	Gly	Met	Gln	Phe	Gly	Leu	Ile	Trp	Asp
			210			215					220				
Gly	Asp	Ser	Val	Glu	Thr	Cys	Ser	Gly	Ala	Phe	Gly	Asp	Tyr	Leu	Lys
225					230					235					240
Phe	Asn	Asn	Pro	His	Lys	Thr	Ser	Leu	Tyr	Leu	Ser	Met	Glu	Leu	Pro
				245					250					255	

Val	Phe	Ile	Trp	Asp	Lys	Ala	Ala	Leu	Ala	Asp	Phe	Ile	Val	Asp	Asn
			260					265					270		
Arg	Ile	Gly	Tyr	Ala	Val	Gly	Ser	Ile	Lys	Glu	Met	Gln	Glu	Ile	Val
		275					280					285			
Asp	Ser	Met	Thr	Ile	Glu	Thr	Tyr	Lys	Gln	Ile	Ser	Glu	Asn	Thr	Lys
	290					295					300				
Ile	Ile	Ser	Gln	Lys	Ile	Arg	Thr	Gly	Ser	Tyr	Phe	Arg	Asp	Val	Leu
305					310					315					320
Glu	Glu	Val	Ile	Asp	Asp	Leu	Lys	Thr	Arg						
				325					330						

<210> 378

<211> 388

<212> PRT

<213> E. Coli

<400> 378

Met	Ile	Tyr	Leu	Val	Ile	Ser	Val	Phe	Leu	Ile	Thr	Ala	Phe	Ile	Cys
1				5					10					15	
Leu	Tyr	Leu	Lys	Lys	Asp	Ile	Phe	Tyr	Pro	Ala	Val	Cys	Val	Asn	Ile
			20					25				30			
Ile	Phe	Ala	Leu	Val	Leu	Leu	Gly	Tyr	Glu	Ile	Thr	Ser	Asp	Ile	Tyr
		35					40					45			
Ala	Phe	Gln	Leu	Asn	Asp	Ala	Thr	Leu	Ile	Phe	Leu	Leu	Cys	Asn	Val
	50				55					60					
Leu	Thr	Phe	Thr	Leu	Ser	Cys	Leu	Leu	Thr	Glu	Ser	Val	Leu	Asp	Leu
65					70				75					80	
Asn	Ile	Arg	Lys	Val	Asn	Asn	Ala	Ile	Tyr	Ser	Ile	Pro	Ser	Lys	Lys
			85					90						95	
Val	His	Asn	Val	Gly	Leu	Leu	Val	Ile	Ser	Phe	Ser	Met	Ile	Tyr	Ile
			100					105					110		
Cys	Met	Arg	Leu	Ser	Asn	Tyr	Gln	Phe	Gly	Thr	Ser	Leu	Leu	Ser	Tyr
		115					120					125			
Met	Asn	Leu	Ile	Arg	Asp	Ala	Asp	Val	Glu	Asp	Thr	Ser	Arg	Asn	Phe
	130					135					140				
Ser	Ala	Tyr	Met	Gln	Pro	Ile	Ile	Leu	Thr	Thr	Phe	Ala	Leu	Phe	Ile
					150					155					160
Trp	Ser	Lys	Lys	Phe	Thr	Asn	Thr	Lys	Val	Ser	Lys	Thr	Phe	Thr	Leu
				165				170						175	
Leu	Val	Phe	Ile	Val	Phe	Ile	Phe	Ala	Ile	Ile	Leu	Asn	Thr	Gly	Lys
			180				185						190		
Gln	Ile	Val	Phe	Met	Val	Ile	Ile	Ser	Tyr	Ala	Phe	Ile	Val	Gly	Val
		195					200					205			
Asn	Arg	Val	Lys	His	Tyr	Val	Tyr	Leu	Ile	Thr	Ala	Val	Gly	Val	Leu
	210					215					220				
Phe	Ser	Leu	Tyr	Met	Leu	Phe	Leu	Arg	Gly	Leu	Pro	Gly	Gly	Met	Ala
225					230					235					240
Tyr	Tyr	Leu	Ser	Met	Tyr	Leu	Val	Ser	Pro	Ile	Ile	Ala	Phe	Gln	Glu
				245					250					255	
Phe	Tyr	Phe	Gln	Gln	Val	Ser	Asn	Ser	Ala	Ser	Ser	His	Val	Phe	Trp
			260				265						270		
Phe	Phe	Glu	Arg	Leu	Met	Gly	Leu	Leu	Thr	Gly	Gly	Val	Ser	Met	Ser
		275				280						285			
Leu	His	Lys	Glu	Phe	Val	Trp	Val	Gly	Leu	Pro	Thr	Asn	Val	Tyr	Thr
	290					295					300				
Ala	Phe	Ser	Asp	Tyr	Val	Tyr	Ile	Ser	Ala	Glu	Leu	Ser	Tyr	Leu	Met

305					310					315				320
Met	Val	Ile	His	Gly	Cys	Ile	Ser	Gly	Val	Leu	Trp	Arg	Leu	Ser
				325					330					335
Asn	Tyr	Ile	Ser	Val	Lys	Ile	Phe	Tyr	Ser	Tyr	Phe	Ile	Tyr	Thr
			340					345					350	
Ser	Phe	Ile	Phe	Tyr	His	Glu	Ser	Phe	Met	Thr	Asn	Ile	Ser	Ser
		355					360				365			Trp
Ile	Gln	Ile	Thr	Leu	Cys	Ile	Ile	Val	Phe	Ser	Gln	Phe	Leu	Lys
	370					375					380			Ala
Gln	Lys	Ile	Lys											
385														

<210> 379
 <211> 367
 <212> PRT
 <213> E. Coli

<400> 379

Met	Tyr	Asp	Tyr	Ile	Ile	Val	Gly	Ser	Gly	Leu	Phe	Gly	Ala	Val	Cys
1				5					10					15	
Ala	Asn	Glu	Leu	Lys	Lys	Leu	Asn	Lys	Lys	Val	Leu	Val	Ile	Glu	Lys
			20					25					30		
Arg	Asn	His	Ile	Gly	Gly	Asn	Ala	Tyr	Thr	Glu	Asp	Cys	Glu	Gly	Ile
		35				40					45				
Gln	Ile	His	Lys	Tyr	Gly	Ala	His	Ile	Phe	His	Thr	Asn	Asp	Lys	Tyr
	50				55					60					
Ile	Trp	Asp	Tyr	Val	Asn	Asp	Leu	Val	Glu	Phe	Asn	Arg	Phe	Thr	Asn
65				70					75					80	
Ser	Pro	Leu	Ala	Ile	Tyr	Lys	Asp	Lys	Leu	Phe	Asn	Leu	Pro	Phe	Asn
			85						90					95	
Met	Asn	Thr	Phe	His	Gln	Met	Trp	Gly	Val	Lys	Asp	Pro	Gln	Glu	Ala
		100						105					110		
Gln	Asn	Ile	Ile	Asn	Ala	Gln	Lys	Lys	Lys	Tyr	Gly	Asp	Lys	Val	Pro
	115					120					125				
Glu	Asn	Leu	Glu	Glu	Gln	Ala	Ile	Ser	Leu	Val	Gly	Glu	Asp	Leu	Tyr
	130				135						140				
Gln	Ala	Leu	Ile	Lys	Gly	Tyr	Thr	Glu	Lys	Gln	Trp	Gly	Arg	Ser	Ala
145				150					155					160	
Lys	Glu	Leu	Pro	Ala	Phe	Ile	Ile	Lys	Arg	Ile	Pro	Val	Arg	Phe	Thr
			165					170					175		
Phe	Asp	Asn	Asn	Tyr	Phe	Ser	Asp	Arg	Tyr	Gln	Gly	Ile	Pro	Val	Gly
		180					185						190		
Gly	Tyr	Thr	Lys	Leu	Ile	Glu	Lys	Met	Leu	Glu	Gly	Val	Asp	Val	Lys
	195					200					205				
Leu	Gly	Ile	Asp	Phe	Leu	Lys	Asp	Lys	Asp	Ser	Leu	Ala	Ser	Lys	Ala
	210				215					220					
His	Arg	Ile	Ile	Tyr	Thr	Gly	Pro	Ile	Asp	Gln	Tyr	Phe	Asp	Tyr	Arg
225				230					235					240	
Phe	Gly	Ala	Leu	Glu	Tyr	Arg	Ser	Leu	Lys	Phe	Glu	Thr	Glu	Arg	His
			245					250					255		
Glu	Phe	Pro	Asn	Phe	Gln	Gly	Asn	Ala	Val	Ile	Asn	Phe	Thr	Asp	Ala
		260					265						270		
Asn	Val	Pro	Tyr	Thr	Arg	Ile	Ile	Glu	His	Lys	His	Phe	Asp	Tyr	Val
	275					280					285				
Glu	Thr	Lys	His	Thr	Val	Val	Thr	Lys	Glu	Tyr	Pro	Leu	Glu	Trp	Lys

290		295		300
Val Gly Asp Glu Pro Tyr Tyr Pro Val Asn Asp Asn Lys Asn Met Glu				
305		310		320
Leu Phe Lys Lys Tyr Arg Glu Leu Ala Ser Arg Glu Asp Lys Val Ile				
		325		335
Phe Gly Gly Arg Leu Ala Glu Tyr Lys Tyr Tyr Asp Met His Gln Val				
		340		350
Ile Ser Ala Ala Leu Tyr Gln Val Lys Asn Ile Met Ser Thr Asp				
		355		365
		360		

<210> 380

<211> 371

<212> PRT

<213> E. Coli

<400> 380

Met Phe Pro Lys Ile Met Asn Asp Glu Asn Phe Phe Lys Lys Ala Ala	
1	5
Ala His Gly Glu Glu Pro Pro Leu Thr Pro Gln Asn Glu His Gln Arg	
	20
Ser Gly Leu Arg Phe Ala Arg Arg Val Arg Leu Pro Arg Ala Val Gly	
	35
Leu Ala Gly Met Phe Leu Pro Ile Ala Ser Thr Leu Val Ser His Pro	
	50
Pro Pro Gly Trp Trp Trp Leu Val Leu Val Gly Trp Ala Phe Val Trp	
65	70
Pro His Leu Ala Trp Gln Ile Ala Ser Arg Ala Val Asp Pro Leu Ser	
	85
Arg Glu Ile Tyr Asn Leu Lys Thr Asp Ala Val Leu Ala Gly Met Trp	
	100
Val Gly Val Met Gly Val Asn Val Leu Pro Ser Thr Ala Met Leu Met	
	115
Ile Met Cys Leu Asn Leu Met Gly Ala Gly Gly Pro Arg Leu Phe Val	
	130
Ala Gly Leu Val Leu Met Val Val Ser Cys Leu Val Thr Leu Glu Leu	
145	150
Thr Gly Ile Thr Val Ser Phe Asn Ser Ala Pro Leu Glu Trp Trp Leu	
	165
Ser Leu Pro Ile Ile Val Ile Tyr Pro Leu Leu Phe Gly Trp Val Ser	
	180
Tyr Gln Thr Ala Thr Lys Leu Ala Glu His Lys Arg Arg Leu Gln Val	
	195
Met Ser Thr Arg Asp Gly Met Thr Gly Val Tyr Asn Arg Arg His Trp	
	210
Glu Thr Met Leu Arg Asn Glu Phe Asp Asn Cys Arg Arg His Asn Arg	
225	230
Asp Ala Thr Leu Leu Ile Ile Asp Ile Asp His Phe Lys Ser Ile Asn	
	245
Asp Thr Trp Gly His Asp Val Gly Asp Glu Ala Ile Val Ala Leu Thr	
	260
Arg Gln Leu Gln Ile Thr Leu Arg Gly Ser Asp Val Ile Gly Arg Phe	
	275
Gly Gly Asp Glu Phe Ala Val Ile Met Ser Gly Thr Pro Ala Glu Ser	
	290
Ala Ile Thr Ala Met Leu Arg Val His Glu Gly Leu Asn Thr Leu Arg	
305	310
	315
	320

Leu	Pro	Asn	Thr	Pro	Gln	Val	Thr	Leu	Arg	Ile	Ser	Val	Gly	Val	Ala
				325					330					335	
Pro	Leu	Asn	Pro	Gln	Met	Ser	His	Tyr	Arg	Glu	Trp	Leu	Lys	Ser	Ala
			340					345					350		
Asp	Leu	Ala	Leu	Tyr	Lys	Ala	Lys	Lys	Ala	Gly	Arg	Asn	Arg	Thr	Glu
		355					360					365			
Val	Ala	Ala													
		370													

<210> 381

<211> 467

<212> PRT

<213> E. Coli

<400> 381

Met	Asp	Val	Asn	Val	Asp	Gln	Phe	Asp	Thr	Glu	Ala	Phe	Arg	Thr	Asp
1				5					10					15	
Lys	Leu	Glu	Leu	Thr	Ser	Gly	Asn	Ile	Ala	Asp	His	Asn	Gly	Asn	Val
			20					25					30		
Val	Ser	Gly	Val	Phe	Asp	Ile	His	Ser	Ser	Asp	Tyr	Val	Leu	Asn	Ala
		35					40					45			
Asp	Leu	Val	Asn	Asp	Arg	Thr	Trp	Asp	Thr	Ser	Lys	Ser	Asn	Tyr	Gly
		50				55					60				
Tyr	Gly	Ile	Val	Ala	Met	Asn	Ser	Asp	Gly	His	Leu	Thr	Ile	Asn	Gly
65					70					75				80	
Asn	Gly	Asp	Val	Asp	Asn	Gly	Thr	Glu	Leu	Asp	Asn	Ser	Ser	Val	Asp
				85					90					95	
Asn	Val	Val	Ala	Ala	Thr	Gly	Asn	Tyr	Lys	Val	Arg	Ile	Asp	Asn	Ala
			100					105					110		
Thr	Gly	Ala	Gly	Ala	Ile	Ala	Asp	Tyr	Lys	Asp	Lys	Glu	Ile	Ile	Tyr
		115					120					125			
Val	Asn	Asp	Val	Asn	Ser	Asn	Ala	Thr	Phe	Ser	Ala	Ala	Asn	Lys	Ala
		130				135					140				
Asp	Leu	Gly	Ala	Tyr	Thr	Tyr	Gln	Ala	Glu	Gln	Arg	Gly	Asn	Thr	Val
145					150					155					160
Val	Leu	Gln	Gln	Met	Glu	Leu	Thr	Asp	Tyr	Ala	Asn	Met	Ala	Leu	Ser
				165					170					175	
Ile	Pro	Ser	Ala	Asn	Thr	Asn	Ile	Trp	Asn	Leu	Glu	Gln	Asp	Thr	Val
			180					185					190		
Gly	Thr	Arg	Leu	Thr	Asn	Ser	Arg	His	Gly	Leu	Ala	Asp	Asn	Gly	Gly
		195					200					205			
Ala	Trp	Val	Ser	Tyr	Phe	Gly	Gly	Asn	Phe	Asn	Gly	Asp	Asn	Gly	Thr
		210				215					220				
Ile	Asn	Tyr	Asp	Gln	Asp	Val	Asn	Gly	Ile	Met	Val	Gly	Val	Asp	Thr
225					230					235					240
Lys	Ile	Asp	Gly	Asn	Asn	Ala	Lys	Trp	Ile	Val	Gly	Ala	Ala	Ala	Gly
				245					250					255	
Phe	Ala	Lys	Gly	Asp	Met	Asn	Asp	Arg	Ser	Gly	Gln	Val	Asp	Gln	Asp
			260					265					270		
Ser	Gln	Thr	Ala	Tyr	Ile	Tyr	Ser	Ser	Ala	His	Phe	Ala	Asn	Asn	Val
		275					280					285			
Phe	Val	Asp	Gly	Ser	Leu	Ser	Tyr	Ser	His	Phe	Asn	Asn	Asp	Leu	Ser
		290				295					300				
Ala	Thr	Met	Ser	Asn	Gly	Thr	Tyr	Val	Asp	Gly	Ser	Thr	Asn	Ser	Asp
305					310					315					320
Ala	Trp	Gly	Phe	Gly	Leu	Lys	Ala	Gly	Tyr	Asp	Phe	Lys	Leu	Gly	Asp
				325					330					335	

Ala Gly Tyr Val Thr Pro Tyr Gly Ser Val Ser Gly Leu Phe Gln Ser
340 345 350
Gly Asp Asp Tyr Gln Leu Ser Asn Asp Met Lys Val Asp Gly Gln Ser
355 360 365
Tyr Asp Ser Met Arg Tyr Glu Leu Gly Val Asp Ala Gly Tyr Thr Phe
370 375 380
Thr Tyr Ser Glu Asp Gln Ala Leu Thr Pro Tyr Phe Lys Leu Ala Tyr
385 390 395 400
Val Tyr Asp Asp Ser Asn Asn Asp Asn Asp Val Asn Gly Asp Ser Ile
405 410 415
Asp Asn Gly Thr Glu Gly Ser Ala Val Arg Val Gly Leu Gly Thr Gln
420 425 430
Phe Ser Phe Thr Lys Asn Phe Ser Ala Tyr Thr Asp Ala Asn Tyr Leu
435 440 445
Gly Gly Gly Asp Val Asp Gln Asp Trp Ser Ala Asn Val Gly Val Lys
450 455 460
Tyr Thr Trp
465

<210> 382
<211> 222
<212> PRT
<213> E. Coli

<400> 382

Met Pro Val Lys Asp Leu Thr Gly Ile Thr Ala Lys Asp Ala Gln Met
1 5 10 15
Leu Ser Val Val Lys Pro Leu Gln Glu Phe Gly Lys Leu Asp Lys Cys
20 25 30
Leu Ser Arg Tyr Gly Thr Arg Phe Glu Phe Asn Asn Glu Lys Gln Val
35 40 45
Ile Phe Ser Ser Asp Val Asn Asn Glu Asp Thr Phe Val Ile Leu Glu
50 55 60
Gly Val Ile Ser Leu Arg Arg Glu Glu Asn Val Leu Ile Gly Ile Thr
65 70 75 80
Gln Ala Pro Tyr Ile Met Gly Leu Ala Asp Gly Leu Met Lys Asn Asp
85 90 95
Ile Pro Tyr Lys Leu Ile Ser Glu Gly Asn Cys Thr Gly Tyr His Leu
100 105 110
Pro Ala Lys Gln Thr Ile Thr Leu Ile Glu Gln Asn Gln Leu Trp Arg
115 120 125
Asp Ala Phe Tyr Trp Leu Ala Trp Gln Asn Arg Ile Leu Glu Leu Arg
130 135 140
Asp Val Gln Leu Ile Gly His Asn Ser Tyr Glu Gln Ile Arg Ala Thr
145 150 155 160
Leu Leu Ser Met Ile Asp Trp Asn Glu Glu Leu Arg Ser Arg Ile Gly
165 170 175
Val Met Asn Tyr Ile His Gln Arg Thr Arg Ile Ser Arg Ser Val Val
180 185 190
Ala Glu Val Leu Ala Ala Leu Arg Lys Gly Gly Tyr Ile Glu Met Asn
195 200 205
Lys Gly Lys Leu Val Ala Ile Asn Arg Leu Pro Ser Glu Tyr
210 215 220

<210> 383
 <211> 84
 <212> PRT
 <213> E. Coli

<400> 383
 Met Thr Asp Lys Ile Arg Thr Leu Gln Gly Arg Val Val Ser Asp Lys
 1 5 10 15
 Met Glu Lys Ser Ile Val Val Ala Ile Glu Arg Phe Val Lys His Pro
 20 25 30
 Ile Tyr Gly Lys Phe Ile Lys Arg Thr Thr Lys Leu His Val His Asp
 35 40 45
 Glu Asn Asn Glu Cys Gly Ile Gly Asp Val Val Glu Ile Arg Glu Cys
 50 55 60
 Arg Pro Leu Ser Lys Thr Lys Ser Trp Thr Leu Val Arg Val Val Glu
 65 70 75 80
 Lys Ala Val Leu

<210> 384
 <211> 63
 <212> PRT
 <213> E. Coli

<400> 384
 Met Lys Ala Lys Glu Leu Arg Glu Lys Ser Val Glu Glu Leu Asn Thr
 1 5 10 15
 Glu Leu Leu Asn Leu Leu Arg Glu Gln Phe Asn Leu Arg Met Gln Ala
 20 25 30
 Ala Ser Gly Gln Leu Gln Gln Ser His Leu Leu Lys Gln Val Arg Arg
 35 40 45
 Asp Val Ala Arg Val Lys Thr Leu Leu Asn Glu Lys Ala Gly Ala
 50 55 60

<210> 385
 <211> 136
 <212> PRT
 <213> E. Coli

<400> 385
 Met Leu Gln Pro Lys Arg Thr Lys Phe Arg Lys Met His Lys Gly Arg
 1 5 10 15
 Asn Arg Gly Leu Ala Gln Gly Thr Asp Val Ser Phe Gly Ser Phe Gly
 20 25 30
 Leu Lys Ala Val Gly Arg Gly Arg Leu Thr Ala Arg Gln Ile Glu Ala
 35 40 45
 Ala Arg Arg Ala Met Thr Arg Ala Val Lys Arg Gln Gly Lys Ile Trp
 50 55 60
 Ile Arg Val Phe Pro Asp Lys Pro Ile Thr Glu Lys Pro Leu Ala Val
 65 70 75 80
 Arg Met Gly Lys Gly Lys Gly Asn Val Glu Tyr Trp Val Ala Leu Ile
 85 90 95
 Gln Pro Gly Lys Val Leu Tyr Glu Met Asp Gly Val Pro Glu Glu Leu
 100 105 110
 Ala Arg Glu Ala Phe Lys Leu Ala Ala Lys Leu Pro Ile Lys Thr
 115 120 125

Thr Phe Val Thr Lys Thr Val Met
130 135

<210> 386
<211> 233
<212> PRT
<213> E. Coli

<400> 386

Met Gly Gln Lys Val His Pro Asn Gly Ile Arg Leu Gly Ile Val Lys
1 5 10 15
Pro Trp Asn Ser Thr Trp Phe Ala Asn Thr Lys Glu Phe Ala Asp Asn
20 25 30
Leu Asp Ser Asp Phe Lys Val Arg Gln Tyr Leu Thr Lys Glu Leu Ala
35 40 45
Lys Ala Ser Val Ser Arg Ile Val Ile Glu Arg Pro Ala Lys Ser Ile
50 55 60
Arg Val Thr Ile His Thr Ala Arg Pro Gly Ile Val Ile Gly Lys Lys
65 70 75 80
Gly Glu Asp Val Glu Lys Leu Arg Lys Val Val Ala Asp Ile Ala Gly
85 90 95
Val Pro Ala Gln Ile Asn Ile Ala Glu Val Arg Lys Pro Glu Leu Asp
100 105 110
Ala Lys Leu Val Ala Asp Ser Ile Thr Ser Gln Leu Glu Arg Arg Val
115 120 125
Met Phe Arg Arg Ala Met Lys Arg Ala Val Gln Asn Ala Met Arg Leu
130 135 140
Gly Ala Lys Gly Ile Lys Val Glu Val Ser Gly Arg Leu Gly Gly Ala
145 150 155 160
Glu Ile Ala Arg Thr Glu Trp Tyr Arg Glu Gly Arg Val Pro Leu His
165 170 175
Thr Leu Arg Ala Asp Ile Asp Tyr Asn Thr Ser Glu Ala His Thr Thr
180 185 190
Tyr Gly Val Ile Gly Val Lys Val Trp Ile Phe Lys Gly Glu Ile Leu
195 200 205
Gly Gly Met Ala Ala Val Glu Gln Pro Glu Lys Pro Ala Ala Gln Pro
210 215 220
Lys Lys Gln Gln Arg Lys Gly Arg Lys
225 230

<210> 387
<211> 110
<212> PRT
<213> E. Coli

<400> 387

Met Glu Thr Ile Ala Lys His Arg His Ala Arg Ser Ser Ala Gln Lys
1 5 10 15
Val Arg Leu Val Ala Asp Leu Ile Arg Gly Lys Lys Val Ser Gln Ala
20 25 30
Leu Asp Ile Leu Thr Tyr Thr Asn Lys Lys Ala Ala Val Leu Val Lys
35 40 45
Lys Val Leu Glu Ser Ala Ile Ala Asn Ala Glu His Asn Asp Gly Ala

50		55		60
Asp Ile Asp Asp Leu Lys Val Thr Lys Ile Phe Val Asp Glu Gly Pro				
65		70		75
Ser Met Lys Arg Ile Met Pro Arg Ala Lys Gly Arg Ala Asp Arg Ile				
	85		90	95
Leu Lys Arg Thr Ser His Ile Thr Val Val Val Ser Asp Arg				
	100		105	110

<210> 388

<211> 92

<212> PRT

<213> E. Coli

<400> 388

Met Pro Arg Ser Leu Lys Lys Gly Pro Phe Ile Asp Leu His Leu Leu				
1	5	10	15	
Met Lys Val Glu Lys Ala Val Glu Ser Gly Asp Lys Lys Pro Leu Arg				
	20	25	30	
Thr Trp Ser Arg Arg Ser Thr Ile Phe Pro Asn Met Ile Gly Leu Thr				
	35	40	45	
Ile Ala Val His Asn Gly Arg Gln His Val Pro Val Phe Val Thr Asp				
	50	55	60	
Glu Met Val Gly His Lys Leu Gly Glu Phe Ala Pro Thr Arg Thr Tyr				
65	70	75	80	
Arg Gly His Ala Ala Asp Lys Lys Ala Lys Lys Lys				
	85	90		

<210> 389

<211> 273

<212> PRT

<213> E. Coli

<400> 389

Met Ala Val Val Lys Cys Lys Pro Thr Ser Pro Gly Arg Arg His Val				
1	5	10	15	
Val Lys Val Val Asn Pro Glu Leu His Lys Gly Lys Pro Phe Ala Pro				
	20	25	30	
Leu Leu Glu Lys Asn Ser Lys Ser Gly Gly Arg Asn Asn Asn Gly Arg				
	35	40	45	
Ile Thr Thr Arg His Ile Gly Gly Gly His Lys Gln Ala Tyr Arg Ile				
	50	55	60	
Val Asp Phe Lys Arg Asn Lys Asp Gly Ile Pro Ala Val Val Glu Arg				
65	70	75	80	
Leu Glu Tyr Asp Pro Asn Arg Ser Ala Asn Ile Ala Leu Val Leu Tyr				
	85	90	95	
Lys Asp Gly Glu Arg Arg Tyr Ile Leu Ala Pro Lys Gly Leu Lys Ala				
	100	105	110	
Gly Asp Gln Ile Gln Ser Gly Val Asp Ala Ala Ile Lys Pro Gly Asn				
	115	120	125	
Thr Leu Pro Met Arg Asn Ile Pro Val Gly Ser Thr Val His Asn Val				
	130	135	140	
Glu Met Lys Pro Gly Lys Gly Gly Gln Leu Ala Arg Ser Ala Gly Thr				
145	150	155	160	

Tyr	Val	Gln	Ile	Val	Ala	Arg	Asp	Gly	Ala	Tyr	Val	Thr	Leu	Arg	Leu
				165					170					175	
Arg	Ser	Gly	Glu	Met	Arg	Lys	Val	Glu	Ala	Asp	Cys	Arg	Ala	Thr	Leu
				180					185					190	
Gly	Glu	Val	Gly	Asn	Ala	Glu	His	Met	Leu	Arg	Val	Leu	Gly	Lys	Ala
				195				200						205	
Gly	Ala	Ala	Arg	Trp	Arg	Gly	Val	Arg	Pro	Thr	Val	Arg	Gly	Thr	Ala
				210				215						220	
Met	Asn	Pro	Val	Asp	His	Pro	His	Gly	Gly	Gly	Glu	Gly	Arg	Asn	Phe
225					230						235				240
Gly	Lys	His	Pro	Val	Thr	Pro	Trp	Gly	Val	Gln	Thr	Lys	Gly	Lys	Lys
				245					250					255	
Thr	Arg	Ser	Asn	Lys	Arg	Thr	Asp	Lys	Phe	Ile	Val	Arg	Arg	Arg	Ser
			260					265						270	

Lys

<210> 390
 <211> 100
 <212> PRT
 <213> E. Coli

<400> 390

Met	Ile	Arg	Glu	Glu	Arg	Leu	Leu	Lys	Val	Leu	Arg	Ala	Pro	His	Val
1				5					10					15	
Ser	Glu	Lys	Ala	Ser	Thr	Ala	Met	Glu	Lys	Ser	Asn	Thr	Ile	Val	Leu
			20					25					30		
Lys	Val	Ala	Lys	Asp	Ala	Thr	Lys	Ala	Glu	Ile	Lys	Ala	Ala	Val	Gln
			35				40					45			
Lys	Leu	Phe	Glu	Val	Glu	Val	Glu	Val	Val	Asn	Thr	Leu	Val	Val	Lys
			50			55					60				
Gly	Lys	Val	Lys	Arg	His	Gly	Gln	Arg	Ile	Gly	Arg	Arg	Ser	Asp	Trp
65					70					75					80
Lys	Lys	Ala	Tyr	Val	Thr	Leu	Lys	Glu	Gly	Gln	Asn	Leu	Asp	Phe	Val
				85					90					95	
Gly	Gly	Ala	Glu												
			100												

<210> 391
 <211> 201
 <212> PRT
 <213> E. Coli

<400> 391

Met	Glu	Leu	Val	Leu	Lys	Asp	Ala	Gln	Ser	Ala	Leu	Thr	Val	Ser	Glu
1				5					10					15	
Thr	Thr	Phe	Gly	Arg	Asp	Phe	Asn	Glu	Ala	Leu	Val	His	Gln	Val	Val
			20					25					30		
Val	Ala	Tyr	Ala	Ala	Gly	Ala	Arg	Gln	Gly	Thr	Arg	Ala	Gln	Lys	Thr
			35				40					45			
Arg	Ala	Glu	Val	Thr	Gly	Ser	Gly	Lys	Lys	Pro	Trp	Arg	Gln	Lys	Gly
			50			55					60				
Thr	Gly	Arg	Ala	Arg	Ser	Gly	Ser	Ile	Lys	Ser	Pro	Ile	Trp	Arg	Ser

65					70					75					80
Gly	Gly	Val	Thr	Phe	Ala	Ala	Arg	Pro	Gln	Asp	His	Ser	Gln	Lys	Val
				85					90					95	
Asn	Lys	Lys	Met	Tyr	Arg	Gly	Ala	Leu	Lys	Ser	Ile	Leu	Ser	Glu	Leu
			100					105					110		
Val	Arg	Gln	Asp	Arg	Leu	Ile	Val	Val	Glu	Lys	Phe	Ser	Val	Glu	Ala
		115					120				125				
Pro	Lys	Thr	Lys	Leu	Leu	Ala	Gln	Lys	Leu	Lys	Asp	Met	Ala	Leu	Glu
	130				135					140					
Asp	Val	Leu	Ile	Ile	Thr	Gly	Glu	Leu	Asp	Glu	Asn	Leu	Phe	Leu	Ala
145				150					155					160	
Ala	Arg	Asn	Leu	His	Lys	Val	Asp	Val	Arg	Asp	Ala	Thr	Gly	Ile	Asp
			165					170						175	
Pro	Val	Ser	Leu	Ile	Ala	Phe	Asp	Lys	Val	Val	Met	Thr	Ala	Asp	Ala
		180					185						190		
Val	Lys	Gln	Val	Glu	Glu	Met	Leu	Ala							
	195						200								

<210> 392
 <211> 209
 <212> PRT
 <213> E. Coli

Met	Ile	Gly	Leu	Val	Gly	Lys	Lys	Val	Gly	Met	Thr	Arg	Ile	Phe	Thr
1				5				10						15	
Glu	Asp	Gly	Val	Ser	Ile	Pro	Val	Thr	Val	Ile	Glu	Val	Glu	Ala	Asn
			20					25					30		
Arg	Val	Thr	Gln	Val	Lys	Asp	Leu	Ala	Asn	Asp	Gly	Tyr	Arg	Ala	Ile
		35					40					45			
Gln	Val	Thr	Thr	Gly	Ala	Lys	Lys	Ala	Asn	Arg	Val	Thr	Lys	Pro	Glu
	50					55					60				
Ala	Gly	His	Phe	Ala	Lys	Ala	Gly	Val	Glu	Ala	Gly	Arg	Gly	Leu	Trp
65				70					75					80	
Glu	Phe	Arg	Leu	Ala	Glu	Gly	Glu	Glu	Phe	Thr	Val	Gly	Gln	Ser	Ile
			85					90					95		
Ser	Val	Glu	Leu	Phe	Ala	Asp	Val	Lys	Lys	Val	Asp	Val	Thr	Gly	Thr
		100					105						110		
Ser	Lys	Gly	Lys	Gly	Phe	Ala	Gly	Thr	Val	Lys	Arg	Trp	Asn	Phe	Arg
	115						120					125			
Thr	Gln	Asp	Ala	Thr	His	Gly	Asn	Ser	Leu	Ser	His	Arg	Val	Pro	Gly
	130					135					140				
Ser	Ile	Gly	Gln	Asn	Gln	Thr	Pro	Gly	Lys	Val	Phe	Lys	Gly	Lys	Lys
145				150					155					160	
Met	Ala	Gly	Gln	Met	Gly	Asn	Glu	Arg	Val	Thr	Val	Gln	Ser	Leu	Asp
			165					170						175	
Val	Val	Arg	Val	Asp	Ala	Glu	Arg	Asn	Leu	Leu	Leu	Val	Lys	Gly	Ala
		180					185						190		
Val	Pro	Gly	Ala	Thr	Gly	Ser	Asp	Leu	Ile	Val	Lys	Pro	Ala	Val	Lys
	195					200						205			
Ala															

<210> 393
 <211> 103
 <212> PRT
 <213> E. Coli

<400> 393
 Met Gln Asn Gln Arg Ile Arg Ile Arg Leu Lys Ala Phe Asp His Arg
 1 5 10 15
 Leu Ile Asp Gln Ala Thr Ala Glu Ile Val Glu Thr Ala Lys Arg Thr
 20 25 30
 Gly Ala Gln Val Arg Gly Pro Ile Pro Leu Pro Thr Arg Lys Glu Arg
 35 40 45
 Phe Thr Val Leu Ile Ser Pro His Val Asn Lys Asp Ala Arg Asp Gln
 50 55 60
 Tyr Glu Ile Arg Thr His Leu Arg Leu Val Asp Ile Val Glu Pro Thr
 65 70 75 80
 Glu Lys Thr Val Asp Ala Leu Met Arg Leu Asp Leu Ala Ala Gly Val
 85 90 95
 Asp Val Gln Ile Ser Leu Gly
 100

<210> 394
 <211> 118
 <212> PRT
 <213> E. Coli

<400> 394
 Met Ala Arg Val Lys Arg Gly Val Ile Ala Arg Ala Arg His Lys Lys
 1 5 10 15
 Ile Leu Lys Gln Ala Lys Gly Tyr Tyr Gly Ala Arg Ser Arg Val Tyr
 20 25 30
 Arg Val Ala Phe Gln Ala Val Ile Lys Ala Gly Gln Tyr Ala Tyr Arg
 35 40 45
 Asp Arg Arg Gln Arg Lys Arg Gln Phe Arg Gln Leu Trp Ile Ala Arg
 50 55 60
 Ile Asn Ala Ala Ala Arg Gln Asn Gly Ile Ser Tyr Ser Lys Phe Ile
 65 70 75 80
 Asn Gly Leu Lys Lys Ala Ser Val Glu Ile Asp Arg Lys Ile Leu Ala
 85 90 95
 Asp Ile Ala Val Phe Asp Lys Val Ala Phe Thr Ala Leu Val Glu Lys
 100 105 110
 Ala Lys Ala Ala Leu Ala
 115

<210> 395
 <211> 65
 <212> PRT
 <213> E. Coli

<400> 395
 Met Pro Lys Ile Lys Thr Val Arg Gly Ala Ala Lys Arg Phe Lys Lys
 1 5 10 15
 Thr Gly Lys Gly Gly Phe Lys His Lys His Ala Asn Leu Arg His Ile
 20 25 30

Leu	Thr	Lys	Lys	Ala	Thr	Lys	Arg	Lys	Arg	His	Leu	Arg	Pro	Lys	Ala
		35					40					45			
Met	Val	Ser	Lys	Gly	Asp	Leu	Gly	Leu	Val	Ile	Ala	Cys	Leu	Pro	Tyr
	50					55					60				
Ala															
65															

<210> 396
 <211> 180
 <212> PRT
 <213> E. Coli

<400> 396

Met	Lys	Gly	Gly	Lys	Arg	Val	Gln	Thr	Ala	Arg	Pro	Asn	Arg	Ile	Asn
1				5					10					15	
Gly	Glu	Ile	Arg	Ala	Gln	Glu	Val	Arg	Leu	Thr	Gly	Leu	Glu	Gly	Glu
			20					25				30			
Gln	Leu	Gly	Ile	Val	Ser	Leu	Arg	Glu	Ala	Leu	Glu	Lys	Ala	Glu	Glu
		35					40					45			
Ala	Gly	Val	Asp	Leu	Val	Glu	Ile	Ser	Pro	Asn	Ala	Glu	Pro	Pro	Val
	50					55				60					
Cys	Arg	Ile	Met	Asp	Tyr	Gly	Lys	Phe	Leu	Tyr	Glu	Lys	Ser	Lys	Ser
65				70						75				80	
Ser	Lys	Glu	Gln	Lys	Lys	Lys	Gln	Lys	Val	Ile	Gln	Val	Lys	Glu	Ile
			85					90					95		
Lys	Phe	Arg	Pro	Gly	Thr	Asp	Glu	Gly	Asp	Tyr	Gln	Val	Lys	Leu	Arg
			100					105					110		
Ser	Leu	Ile	Arg	Phe	Leu	Glu	Glu	Gly	Asp	Lys	Ala	Lys	Ile	Thr	Leu
		115					120					125			
Arg	Phe	Arg	Gly	Arg	Glu	Met	Ala	His	Gln	Gln	Ile	Gly	Met	Glu	Val
		130				135					140				
Leu	Asn	Arg	Val	Lys	Asp	Asp	Leu	Gln	Glu	Leu	Ala	Val	Val	Glu	Ser
145				150						155				160	
Phe	Pro	Thr	Lys	Ile	Glu	Gly	Arg	Gln	Met	Ile	Met	Val	Leu	Ala	Pro
			165					170						175	
Lys	Lys	Lys	Gln												
			180												

<210> 397
 <211> 642
 <212> PRT
 <213> E. Coli

<400> 397

Met	Pro	Val	Ile	Thr	Leu	Pro	Asp	Gly	Ser	Gln	Arg	His	Tyr	Asp	His
1				5					10					15	
Ala	Val	Ser	Pro	Met	Asp	Val	Ala	Leu	Asp	Ile	Gly	Pro	Gly	Leu	Ala
			20					25					30		
Lys	Ala	Cys	Ile	Ala	Gly	Arg	Val	Asn	Gly	Glu	Leu	Val	Asp	Ala	Cys
		35					40					45			
Asp	Leu	Ile	Glu	Asn	Asp	Ala	Gln	Leu	Ser	Ile	Ile	Thr	Ala	Lys	Asp
	50					55					60				
Glu	Glu	Gly	Leu	Glu	Ile	Ile	Arg	His	Ser	Cys	Ala	His	Leu	Leu	Gly

65	His	Ala	Ile	Lys	Gln	Leu	Trp	Pro	His	Thr	Lys	Met	Ala	Ile	Gly	Pro	80
					85					90					95		
Val	Ile	Asp	Asn	Gly	Phe	Tyr	Tyr	Asp	Val	Asp	Leu	Asp	Arg	Thr	Leu		
			100					105					110				
Thr	Gln	Glu	Asp	Val	Glu	Ala	Leu	Glu	Lys	Arg	Met	His	Glu	Leu	Ala		
		115					120					125					
Glu	Lys	Asn	Tyr	Asp	Val	Ile	Lys	Lys	Lys	Val	Ser	Trp	His	Glu	Ala		
	130					135					140						
Arg	Glu	Thr	Phe	Ala	Asn	Arg	Gly	Glu	Ser	Tyr	Lys	Val	Ser	Ile	Leu		
145					150					155					160		
Asp	Glu	Asn	Ile	Ala	His	Asp	Asp	Lys	Pro	Gly	Leu	Tyr	Phe	His	Glu		
			165						170					175			
Glu	Tyr	Val	Asp	Met	Cys	Arg	Gly	Pro	His	Val	Pro	Asn	Met	Arg	Phe		
		180					185						190				
Cys	His	His	Phe	Lys	Leu	Met	Lys	Thr	Ala	Gly	Ala	Tyr	Trp	Arg	Gly		
	195					200						205					
Asp	Ser	Asn	Asn	Lys	Met	Leu	Gln	Arg	Ile	Tyr	Gly	Thr	Ala	Trp	Ala		
	210				215						220						
Asp	Lys	Lys	Ala	Leu	Asn	Ala	Tyr	Leu	Gln	Arg	Leu	Glu	Glu	Ala	Ala		
225				230					235					240			
Lys	Arg	Asp	His	Arg	Lys	Ile	Gly	Lys	Gln	Leu	Asp	Leu	Tyr	His	Met		
			245				250						255				
Gln	Glu	Glu	Ala	Pro	Gly	Met	Val	Phe	Trp	His	Asn	Asp	Gly	Trp	Thr		
			260				265						270				
Ile	Phe	Arg	Glu	Leu	Glu	Val	Phe	Val	Arg	Ser	Lys	Leu	Lys	Glu	Tyr		
	275					280						285					
Gln	Tyr	Gln	Glu	Val	Lys	Gly	Pro	Phe	Met	Met	Asp	Arg	Val	Leu	Trp		
	290				295						300						
Glu	Lys	Thr	Gly	His	Trp	Asp	Asn	Tyr	Lys	Asp	Ala	Met	Phe	Thr	Thr		
305				310					315					320			
Ser	Ser	Glu	Asn	Arg	Glu	Tyr	Cys	Ile	Lys	Pro	Met	Asn	Cys	Pro	Gly		
			325				330						335				
His	Val	Gln	Ile	Phe	Asn	Gln	Gly	Leu	Lys	Ser	Tyr	Arg	Asp	Leu	Pro		
		340				345						350					
Leu	Arg	Met	Ala	Glu	Phe	Gly	Ser	Cys	His	Arg	Asn	Glu	Pro	Ser	Gly		
	355					360						365					
Ser	Leu	His	Gly	Leu	Met	Arg	Val	Arg	Gly	Phe	Thr	Gln	Asp	Asp	Ala		
	370				375						380						
His	Ile	Phe	Cys	Thr	Glu	Glu	Gln	Ile	Arg	Asp	Glu	Val	Asn	Gly	Cys		
385				390					395					400			
Ile	Arg	Leu	Val	Tyr	Asp	Met	Tyr	Ser	Thr	Phe	Gly	Phe	Glu	Lys	Ile		
			405				410						415				
Val	Val	Lys	Leu	Ser	Thr	Arg	Pro	Glu	Lys	Arg	Ile	Gly	Ser	Asp	Glu		
		420					425					430					
Met	Trp	Asp	Arg	Ala	Glu	Ala	Asp	Leu	Ala	Val	Ala	Leu	Glu	Glu	Asn		
	435					440						445					
Asn	Ile	Pro	Phe	Glu	Tyr	Gln	Leu	Gly	Glu	Gly	Ala	Phe	Tyr	Gly	Pro		
	450				455						460						
Lys	Ile	Glu	Phe	Thr	Leu	Tyr	Asp	Cys	Leu	Asp	Arg	Ala	Trp	Gln	Cys		
465				470					475					480			
Gly	Thr	Val	Gln	Leu	Asp	Phe	Ser	Leu	Pro	Ser	Arg	Leu	Ser	Ala	Ser		
			485					490					495				
Tyr	Val	Gly	Glu	Asp	Asn	Glu	Arg	Lys	Val	Pro	Val	Met	Ile	His	Arg		
		500				505						510					
Ala	Ile	Leu	Gly	Ser	Met	Glu	Arg	Phe	Ile	Gly	Ile	Leu	Thr	Glu	Glu		
	515					520						525					

Phe	Ala	Gly	Phe	Phe	Pro	Thr	Trp	Leu	Ala	Pro	Val	Gln	Val	Val	Ile
530						535					540				
Met	Asn	Ile	Thr	Asp	Ser	Gln	Ser	Glu	Tyr	Val	Asn	Glu	Leu	Thr	Gln
545					550					555					560
Lys	Leu	Ser	Asn	Ala	Gly	Ile	Arg	Val	Lys	Ala	Asp	Leu	Arg	Asn	Glu
			565						570					575	
Lys	Ile	Gly	Phe	Lys	Ile	Arg	Glu	His	Thr	Leu	Arg	Arg	Val	Pro	Tyr
			580					585					590		
Met	Leu	Val	Cys	Gly	Asp	Lys	Glu	Val	Glu	Ser	Gly	Lys	Val	Ala	Val
	595						600					605			
Arg	Thr	Arg	Arg	Gly	Lys	Asp	Leu	Gly	Ser	Met	Asp	Val	Asn	Glu	Val
610						615					620				
Ile	Glu	Lys	Leu	Gln	Gln	Glu	Ile	Arg	Ser	Arg	Ser	Leu	Lys	Gln	Leu
625					630					635					640
Glu	Glu														

<210> 398
 <211> 450
 <212> PRT
 <213> E. Coli

<400> 398

Met	Thr	Lys	His	Tyr	Asp	Tyr	Ile	Ala	Ile	Gly	Gly	Gly	Ser	Gly	Gly
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		20					25						30		
Ile	Glu	Ala	Lys	Glu	Leu	Gly	Gly	Thr	Cys	Val	Asn	Val	Gly	Cys	Val
	35					40						45			
Pro	Lys	Lys	Val	Met	Trp	His	Ala	Ala	Gln	Ile	Arg	Glu	Ala	Ile	His
50					55						60				
Met	Tyr	Gly	Pro	Asp	Tyr	Gly	Phe	Asp	Thr	Thr	Ile	Asn	Lys	Phe	Asn
65				70						75					80
Trp	Glu	Thr	Leu	Ile	Ala	Ser	Arg	Thr	Ala	Tyr	Ile	Asp	Arg	Ile	His
			85						90					95	
Thr	Ser	Tyr	Glu	Asn	Val	Leu	Gly	Lys	Asn	Asn	Val	Asp	Val	Ile	Lys
			100					105					110		
Gly	Phe	Ala	Arg	Phe	Val	Asp	Ala	Lys	Thr	Leu	Glu	Val	Asn	Gly	Glu
	115						120					125			
Thr	Ile	Thr	Ala	Asp	His	Ile	Leu	Ile	Ala	Thr	Gly	Gly	Arg	Pro	Ser
130						135					140				
His	Pro	Asp	Ile	Pro	Gly	Val	Glu	Tyr	Gly	Ile	Asp	Ser	Asp	Gly	Phe
145					150					155					160
Phe	Ala	Leu	Pro	Ala	Leu	Pro	Glu	Arg	Val	Ala	Val	Val	Gly	Ala	Gly
			165						170					175	
Tyr	Ile	Ala	Val	Glu	Leu	Ala	Gly	Val	Ile	Asn	Gly	Leu	Gly	Ala	Lys
		180					185						190		
Thr	His	Leu	Phe	Val	Arg	Lys	His	Ala	Pro	Leu	Arg	Ser	Phe	Asp	Pro
	195					200						205			
Met	Ile	Ser	Glu	Thr	Leu	Val	Glu	Val	Met	Asn	Ala	Glu	Gly	Pro	Gln
	210					215					220				
Leu	His	Thr	Asn	Ala	Ile	Pro	Lys	Ala	Val	Val	Lys	Asn	Thr	Asp	Gly
225					230					235					240
Ser	Leu	Thr	Leu	Glu	Leu	Glu	Asp	Gly	Arg	Ser	Glu	Thr	Val	Asp	Cys
			245						250					255	
Leu	Ile	Trp	Ala	Ile	Gly	Arg	Glu	Pro	Ala	Asn	Asp	Asn	Ile	Asn	Leu

caucacgccu	cagccuugau	uuuccggauu	ugccuggaaa	accagccuac	acgcuuaaac	1440
cgggacaacc	gucgcccggc	caacauagcc	uucuccgucc	ccccuucgca	guaacaccaa	1500
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gcuccccguu	cgcucgccgc	uacuggggga	aucucgguug	auuucuuuuc	cucggggguac	2700
uuagauguuu	caguuccccc	gguucgccuc	auuaaccuau	ggauucaguu	aaugauagug	2760
ugucgaaaca	cacugggguu	ccccauucgg	aaauccggcg	uuauaacggu	ucauauaccc	2820
uuaccgacgc	uuauccgaga	uuagcacguc	cuucaucgcc	ucugacugcc	agggcaucca	2880
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<210> 400

<211> 120

<212> RNA

<213> E. Coli

<400> 400

augccuggca	guucccuacu	cucgcauggg	gagacccac	acuaccaucg	gcgcuacggc	60
guuucacuuc	ugaguucggc	auggggucag	gugggaccac	cgcgcuacgg	ccgccaggca	120

<210> 401

<211> 76

<212> RNA

<213> E. Coli

<400> 401

gucccccucg	ucuagaggcc	caggacaccg	cccuuucacg	gcgguaacag	ggguucgaau	60
ccccuagggg	acgccca					76

<210> 402

<211> 1549

<212> RNA

<213> E. Coli

<400> 402

aaauugaaga	guuugaucau	ggcucagauu	gaacgcuggc	ggcaggccua	acacaugcaa	60
gucgaacggu	aacaggaagc	agcuugcugc	uucgcugacg	aguggcggac	gggugaguaa	120
ugucugggaa	gcugccugau	ggagggggau	aacuacugga	aacgguagcu	aauaccgcau	180
aaugucgcaa	gaccaaagag	ggggaccuuc	gggccucuug	ccaucggaug	ugcccagaug	240
ggauuagcuu	guuggugggg	uaacggcuca	ccaaggcgac	gaucccuagc	uggucugaga	300
ggaugaccag	ccacacugga	acugagacac	gguccagacu	ccuacgggag	gcagcagugg	360
ggaauauugc	acaaugggag	caagccugau	gcagccaugc	cgcguguau	aagaaggccu	420
ucggguugua	aaguacuuc	agcggggagg	aagggaguaa	aguuaauacc	uuugcucauu	480
gacguuaccc	gcagaagaag	caccggcuua	cuccgugcca	gcagccgagg	uaauacggag	540
ggugcaagcg	uuauucggaa	uuacugggcg	uaaagcgcac	gcagggcggu	ugguuaaguc	600
agaugugaaa	uccccgggcu	caaccuggga	acugcaucug	auacuggcaa	gcuugagucu	660
cguagagggg	gguagaauc	cagguguagc	ggugaaaugc	guagagauuc	ggaggaauc	720
cgguggcgaa	ggcgggccccc	uggacgaaga	cugacgcuca	ggugcgaaag	cguggggagc	780
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ccuugagggc	uggcuuccgg	agcuaacgcg	uuagucgac	cgcuggggga	guacggccgc	900
aagguuaaaa	cucaaaugaa	uugacggggg	cccgcacaag	cgguggagca	ugugguuuaa	960
uucgaugcaa	cgcaagaac	cuuaccuggu	cuugacaucc	acggaaguuu	ucagagauga	1020
gaaugugccu	ucgggaaccg	ugagacaggu	gcugcauggc	ugucgucagc	ucguguugug	1080
aaauguuggg	uuagucccg	caacgagcgc	aaccuuuau	cuuuguugcc	agcgguccgg	1140
ccgggaacuc	aaaggagacu	gccagugaua	aacuggagga	agguggggau	gacgucaagu	1200
caucauggcc	cuuacgacca	gggcuacaca	cgugcuacaa	uggcgcauac	aaagagaagc	1260
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uucccgggcc	uuguacacac	cgcccugcac	accaugggag	uggguugcaa	aagaaguagg	1440
uagcuuaacc	uucgggaggg	cgcuuaccac	uuugugauuc	augacugggg	ugaagucgua	1500
acaagguaac	cguaggggaa	ccugcggguu	gaucaccucc	uuaccuuaa		1549

<210> 403

<211> 17

<212> DNA

<213> Artificial

<220>

<223> Primer Oligonucleotide

<400> 403

tgtttatcag accgctt

17

<210> 404

<211> 18

<212> DNA

<213> Artificial

<220>

<223> Primer Oligonucleotide

<400> 404

acaatttcac acagcctc

18

<210> 405

<211> 159

<212> DNA

<213> Escherichia coli

<400> 405
caggtggtat ggaaacccaa aatggagacg ggaagctgaa ccagatagtt actggaggtg 60
atcaccagca gatgaaataa cgataaccag aacaacgcct tatagcgttg agtttgcgag 120
aaaacgttca tattgtacct ttttgattaa ccattgggg 159

<210> 406
<211> 640
<212> DNA
<213> Escherichia coli

<220>
<221> misc_feature
<222> (1)...(640)
<223> n = A,T,C or G

<400> 406
ggggnccaaa gtgtttgggn cgggcaactg gaggccaacc ttaanttnng ggaaatTTTT 60
aanaaaaggc ggggatttgt nagccacggg ngattanttt anaataaatt aagtgttgcc 120
ataaggggac aaagngaagg aagtggntat taanggannc gccaatgcga nttagggcag 180
accattcggc cattcgcctt cttggttatt gaagttcatc cagatagccg ttgcengacc 240
gaccagattc gcttcnggca caaagcccca gtaacggctg tccgcgctgt tgcgcgggtt 300
gtcgcctatc atgaagtatt gtcccggagg aacaatccag gttgccagtt gttgccctgg 360
ctgctggtaa tacatcccca cctgatcctg cgcaatcggc actgtcagaa tgcggtgcgt 420
cacatcacc cagtgtctctt tacgctcgga aagacgaatt ccattttctt tggtttcgtt 480
tttcggcact tcaaagaatc cgctggctgc ttccccacca ttacggcgtg agaaggtctg 540
aacgaaatcg ctcggttcca cgtttgagta ggtgaccggc agcgcgtttt cacacgcctg 600
gccggaactg catcccgggt gaatcgtcag ctcttttgag 640

<210> 407
<211> 682
<212> DNA
<213> Escherichia coli

<220>
<221> misc_feature
<222> (1)...(682)
<223> n = A,T,C or G

<400> 407
cctgcagggt aatgtcgcca ttaaactggc gcaggcagcc aaagagttgc tccgcttcta 60
cccagtcggc agcgacaact tgcgttaaag tcgcaaaatt atcatctgca ctcaactgcgt 120
gacgtaagcg gatggagtgg ccggaacct catagtacc gccaccagt tggcctgcat 180
cgctttgtag cgtacgcgcg gcattggcaa taagattcag atactcagac tcttccgggg 240
ccttcgccag cataaaagag gaggatgctc gcgtatgcag caactgctcc agcgcaaatt 300
gcagccgcgg ttgagtatca ctgaataaag gatcgttttc gtcaatcaaa tgtggctgag 360
caaatatatt ctgatagcta tcggtatcag gaaccaggct acgccatgca agtttcgtaa 420
tggtcaaagt tgatgttttt tagtctgttg tcaaagccgc nattataccn gtaaccggca 480
ctacagcaca cgtagaaagc acccgacaat actcctggca tgggcgttaa agctcacagg 540
atggagatct tttcttcact ggcctaaaaa gctgatattc tgtaaagagt tacacngtaa 600
cattgagatc gctatgaaat atcaacaact tggaaaatct tgnaaagcng gttggaaaaa 660
ggaaagtatc tggttaagaa gc 682

<210> 408
<211> 309
<212> DNA
<213> Escherichia coli

<400> 408
 ggggatccgg cagaatttta cgctgaccaa tgacgcgacg acgtggcatg gaaatactcc 60
 gttgttaatt caggattgtc caaaactcta cgagtttagt ttgacattta agttaaaccg 120
 tttggcctta cttaacggag aaccattaag ccttaggacg cttcacgcca tacttggaac 180
 gagcctgctt acgggtcttta acgccggagc agtcaagcgc accacgtacg gtgtggtaac 240
 gaacacccgg gaggtcttta acacgaccgc cacggatcag gatcacggag tgctcctgca 300
 gccaaagctt 309

<210> 409
 <211> 1167
 <212> DNA
 <213> Escherichia coli

<400> 409
 gtcgacccat ctgtccattg agcggacagt ttgtgcaaca ctatatttgtt gaccggaaaa 60
 tggaacactt tccgcaatgc ctgttgctat cacgcttaaa ccatttcatt gcgatttaca 120
 cagaacggac gtcctgtcgc agtatattaa gtcgtcgata gaaacaagca ttgaaaggca 180
 cagcagtagt caaacagtgt gaaacgctac tggcgccctta cagcgcaaaa aggctgggtga 240
 ctaaaaagtc accagccatc agcctgattt ctcaggctgc aaccggaagg gttggcttat 300
 ttaacttcaa cttcagcgcc agcttcttcc agagcttttt tcagtgtctc tgcgtcgtct 360
 ttgctcacgc cttctttcag agcagccggt gcagattcta ccaggctctt agcttctttc 420
 agaccaggc cagttgcgcc acgtactgct ttgataacag caactttgtt agcgccagca 480
 gctttcagaa ttacgtcgaa ttcagttttt tcttcagcag cttcaaccgg gccagcagct 540
 acagctacag cagcagcagc ggaaacaccg aatttttctt ycattgcaga gatcaagttc 600
 tacaacgtcc attacagaca tagctgcaac tgcttcaatg awttgatctt tagtgataga 660
 catttaaatk gttcctgaat atcagaataa gtttatacgt aagcgaatgc gttaaaaaga 720
 taactgcgaw taagcagctt ytttcgcac gcgtacagma gccagagtac gaaccagttt 780
 gccagccgaa gcttctttca tgggtggccat caggcgtgca attgcttctt cgtaggtcgg 840
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 tttgacctca aattttgcat tcgctttcgc gaactctttg aacagacgag cagcagcggc 960
 cgggtgttcc atagagtatg caatcagggg cggaccaaca aacgcgtctt tcaggcactc 1020
 gaacggagta ctttcaacag cacggcgcag cagggtgtta cgaacaacac gcatgtatac 1080
 gccagcttcg cgacctgctt tacgcagttc agtcatttta tctacagtta cgcccacggg 1140
 aatccgcaac tactgcaagc caagctt 1167

<210> 410
 <211> 404
 <212> DNA
 <213> Escherichia coli

<400> 410
 caacmctatt ttgktggacc ggaaaakgga acactttccg cawkgcctgt tgctatcacg 60
 cttaaaccat ttcattgcga tttacacaga acggacgtcc tgcgcgagta tattaagtcg 120
 tcgatagaaa caagcattga aaggcacagc agtagtcaaa cagtgtgaaa cgctactggc 180
 gccttacagc gcaaaaaggc tggtgactaa aaagtcacca gccatcagcc tgattttctca 240
 ggctgcaacc ggaagggttg gcttatttaa cttcaacttc agcgccagct tcttcagag 300
 cttttttcag tgcttctgcg tcgtctttgc tcacgccttc tttcagagca gccggtgcag 360
 attctaccag gtcttttagct tctttcagac ccaggccagt tgcg 404

<210> 411
 <211> 152
 <212> DNA
 <213> Escherichia coli

<400> 411
 agagcttttt tcagtgtctc tgcgtcgtct ttgctcacgc cttctttcaa gagcagcccg 60
 gtgcagattc taccaggtct ttagcttctt tcagaccag gccagttgcg ccacgtactg 120

ctttgataac agcaactttg ttagcgccag ca

152

<210> 412

<211> 825

<212> DNA

<213> Escherichia coli

<220>

<221> misc_feature

<222> (1)...(825)

<223> n = A,T,C or G

<400> 412

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ttacacagaa	cggacgtcct	gtcgcagtat	attaagtcgt	cgatagaaac	aagcattgaa	180
aggcacagca	gtagtcaaac	agtgtgaaac	gctactggcg	ccttacagcg	caaaaaggct	240
ggtgactaaa	aagtcaccag	ccatcagcct	gatttctcag	gctgcaaccg	gaagggttgg	300
cttattttaac	ttcaacttca	gcgccagctt	cttccagagc	ttttttcagt	gcttctgcgt	360
cgtcttttgc	cacgccttct	ttcagagcag	ccgggtgcag	attctaccag	gtcttttagct	420
tcttttcagac	ccaggccagt	tgccgccacgt	actgctttga	taacagcaac	ttgttttagcg	480
ccagcagctt	tcagaattac	gtcgaattca	agttttttct	tcagcagctt	caaccgggcc	540
agcagctaca	gctacagcag	cagcagcgga	aacaccgaat	ttttcttyca	ttggcagaga	600
tcaagttcta	caacgtccat	tacagacata	gctgcaactg	cttcaatgat	tkgatcttwa	660
gtgatagaca	tttaaattgt	tcctgaatat	cagaataagt	ttatacgtaa	gcgaatgcgt	720
taaaaagata	actgcgatta	agcagcttct	ttcgcacgcg	gtacagcagc	cagaggctcg	780
accagtttgc	cagccgaagg	ttggcttttc	agcctnnncn	natta		825

<210> 413

<211> 425

<212> DNA

<213> Escherichia coli

<400> 413

agtagtcaaa	caggtgkgra	acgctactgg	cgccttacag	cgcaaaaagg	ctggtgacta	60
aaaagtcacc	agccatcarc	ctgatttctc	aggctgcaac	ccggaagggt	tggcttattt	120
aacttcaact	tcagcgccag	cttcttccag	agcttttttc	agtgcctctg	cgtcgtcttt	180
gctcacgcct	tctttcagag	cagccggtgc	agattctacc	aggtcttttag	cttctttcag	240
acccaggcca	gttgcgccac	gtactgcttt	gataacagca	actttgttag	cgccagcagc	300
tttcagaatt	acgtcgaatt	cagttttttc	ttcagcagct	tcaaccgggc	cagcagctac	360
agctacagca	gcagcagcgg	aaacaccgga	atttttcttc	cattgcagag	atcaagttct	420
acaac						425

<210> 414

<211> 126

<212> DNA

<213> Escherichia coli

<400> 414

agagcttttt	tcagtgtctc	tgcgctcgtc	ttgctcacgc	cttcttttcag	agcagccgggt	60
gcagattcta	ccaggtcttt	agcttctttc	agaccagggc	cagttgcgcc	acgtactgct	120
ttrata						126

<210> 415

<211> 264

<212> DNA

<213> Escherichia coli

<400> 415
ctgcmacccg garggggttg cttattttaac ttcaacttca gcgccagctt cttycagagc 60
ttttttcaag tgcttctgcg tcgtctttgc tcacgccttc tttcagagca gccggtgcag 120
attctaccag gtcttttagct tctttcagac ccaggccagt tgcgccacgt actgctttga 180
taacagcaac tttgttagcg ccagcagctt tcagaattac gtcgaattca gttttttctt 240
cagcagcttc aaccgggcca gcag 264

<210> 416
<211> 201
<212> DNA
<213> Escherichia coli

<400> 416
cgcataccct gcagcatcgg cccgatggag atcagggtcgg cagaacgctg taccgctttg 60
taggtggtgt taccggtggt cagatccggg aagatgaaca cggtagcgcg acctgcaacc 120
ggagagttcg gcgctttgga tttcgcaacg tcagccatta ccgcagcgtc gtactgcagc 180
ggaccgtcga tcacaggtc a 201

<210> 417
<211> 239
<212> DNA
<213> Escherichia coli

<400> 417
aattcagcag ttgacagtgg cataaacgta actggtgact tttgccggc atgacgccgg 60
gcttttttta ttattccgtg acttccagcg tagtgaaggc aaacttctcg ccatcaaata 120
gcccctgact ggtagtttt agcgcgggga tcaactggcag agaaagaaac gccatctgaa 180
taaacggctc atcgggtaac ggaccgcatt cacgggcggc ggctttcaag gcgtcaatt 239

<210> 418
<211> 223
<212> DNA
<213> Escherichia coli

<400> 418
ttcttttttt cgtcaacggg gtccagaatc attttattta cctcgggtac ttatgctgat 60
ttttattatt atggggaagg tgttatttat gagtttcatt tatgccgtaa cgacaatgaa 120
ctcgggaatt agtataagca gcgcgagaat aataatcatt gtgcaaatgc taatttaatt 180
aatactattt aaatattatt ttgagcatat gcacataagg ttg 223

<210> 419
<211> 223
<212> DNA
<213> Escherichia coli

<400> 419
ttcttttttt cgtcaacggg gtccagaatc attttattta cctcgggtac ttatgctgat 60
ttttattatt atggggaagg tgttatttat gagtttcatt tatgccgtaa cgacaatgaa 120
ctcgggaatt agtataagca gcgcgagaat aataatcatt gtgcaaatgc taatttaatt 180
aatactattt aaatattatt ttgagcatat gcacataagg ttg 223

<210> 420
<211> 212
<212> DNA
<213> Escherichia coli

<400> 420
aatagcgggt atgcacgcct ttcttttttt cgtcaacggt gtccagaatc attttattta 60
cctcgggtac ttatgctgat ttttattatt atggggaagg tgttatttat gagtttcatt 120
tatgccgtaa cgmcaatgaa ctcggaatt agtataagca gcgcgagaat aataatcatt 180
gtgcaaatgc taatttaatt aatactattt aa 212

<210> 421
<211> 438
<212> DNA
<213> Escherichia coli

<400> 421
ccctgtaaat tatcgcccgt ggcataaaaa ctgctgccaa acgccgtctt tgccagcagc 60
caggccataa atgccaccag aattatcgct aaccaaccaa ttgctgaaac gccaaagcagc 120
agcggggcgg agagctgttt cagttcggcg ggtaaccctt caatccattt gccgccagtc 180
cacagcaaca tgatgcctct gtacaaccct aacgtgccaa ggggtggcaac aatggcaggg 240
atcttttagcc acgcgaccag gacaccgttg aaaaatcccg cgagcaaacc aagcagtaaa 300
gtcgcgacac aagcaacagg tagtgaatat cctgcgttca gtaacatccc caacagcacc 360
gcgcacattc cgggtaatcg aacccactt gaaacatcaa tattgsgsgt aagcattwcc 420
aagcgttcgs gcccatkg 438

<210> 422
<211> 682
<212> DNA
<213> Escherichia coli

<400> 422
aattcccggg gatccgtcga ccgtgcgctt ccggttggtg caaccgcga aatggcgcg 60
cggtaaagtat ggcgggggta ttcttcccc gttgaggaca ccgggttgct aggttgacca 120
tacgcttaag tgacaacccc gctgcaacgc cctctgttat caattttctg gtgacgtttg 180
gcggtatcag ttttactccg tgactgctct gccgcccttt ttaaagtga tttgtgatg 240
tggtgaatgc ggctgagcgc acgcggaaca gttaaaacca aaacagtgat tatgggtgga 300
ttctctgtat ccggcggttaa ttgttaactg gttaacgtca cctggaggca ccaggcactg 360
catcacaaaa ttcattgttg aggacgcgat aatgaaaacg ttattaccaa acgttaatac 420
gtctgaaggt tgttttgaaa ttggtgtcac tatcagtaac ccagtattta ctgaagatgc 480
cattaacaag agaaaacaag aacgggagct attaaataaa atatgcattg tttcaatgct 540
ggctcgttta cgtctgatgc caaaaggatg tgcacaatga attcagcatt tgtgcttgtt 600
ctgacagttt ttcttgtttc cggagagcca gttgatattg cagtcagtgat tcacaggaca 660
atgcaggagt gatgactgca gc 682

<210> 423
<211> 600
<212> DNA
<213> Escherichia coli

<400> 423
ggggatccga ttgtgactgc tctgccgccc tttttaaagt gaattttgtg atgtggtgaa 60
tgcggtctgag cgcacgcgga acagttaaaa ccaaaaacag tggtatgggt ggattctctg 120
tatccggcgt taattgttaa ctggttaacg tcacctggag gcaccaggca ctgcatcaca 180
aaattcattg ttgaggacgc gataatgaaa acgttattac caaacgttaa tacgtctgaa 240
ggttgttttg aaattgggtg cactatcagt aaccagtat ttactgaaga tgccattaac 300
aagagaaaaa aagaacggga gctattaaat aaaaattgca ttgtttcaat gctggctcgt 360
ttacgtctga tgccaaaagg atgtgcacaa tgaattcagc atttgtgctt gttctgacag 420
tttttcttgt ttccggagag ccagttgata ttgcagtcag tgttcacagg acaatgcagg 480
agtgtatgac tgcagcaacc gaacagaaaa ttcccggtaa ctgttaccgg gtcgataaag 540
ttattcacca ggataatatc gaaatcccg cagggtcttta aacagttccg taataaataa 600

<210> 424
 <211> 100
 <212> DNA
 <213> Escherichia coli

<400> 424
 gggatccagc aagaagatgc gggtgtaccg tcatcacgca gatgcgcaaa gctactcagc 60
 aactgacctt tcttcgcaat aagcacgcca ttagcgatcat 100

<210> 425
 <211> 465
 <212> DNA
 <213> Escherichia coli

<400> 425
 tcgcgtgttt accttcaaca tcggtaactt tctggcggat agtttcacgg taagcaacct 60
 gcggtttacc tacgttcgct tcaacgttga attcacgctt catacgggtca acgatgatgt 120
 cgagggtcag ttcgcccata cccgcgatga tggctctggt agattcttcg tcagtccata 180
 cacggaaaga cgggtcttct ttagccagac ggcccagagc cagaccatt ttttcctggt 240
 cagctttggt tttcgggttca actgcgatgg agattaccgg ctccagggaat tccatacgtt 300
 ccagaatgat cggcgcaccc gggtcacaca ggggtgcacc agtgggttacg tctttcagac 360
 cgatagcagc agcgatgtcg cccgcgcgaa cttctttgat ctcttcacgt ttgttagcgt 420
 gcatctgaac gatacgaccg aaacgctcac gtgcagcttt cacgg 465

<210> 426
 <211> 653
 <212> DNA
 <213> Escherichia coli

<220>
 <221> misc_feature
 <222> (1)...(653)
 <223> n = A,T,C or G

<400> 426
 tgatcggctc aagcagaact gggttcgctt tcttaaagcc ttctttaaag gcgatagaag 60
 cagccagttt aaacgccagt tcagaggagt caacgtcatg gtaagaaccg aagtgcagac 120
 gaatacccat gtctactacc gggtagcctg ccagcggacc tgctttcagc tgttcctgga 180
 tacctttatc aacggccggg atgtattcgc cagggattac accaccttta atgtcgttga 240
 tgaactcgta gcctttcggg tttgaaccgc gctccagcgg gtacatgtcg ataacaacat 300
 gaccatactg accacgacca ccagactgtt tcgcgtgttt accttcaaca tcggtaactt 360
 tctggcggat agtttcacgg taagcaacct gcggtttacc tacgttcgct tcaacgttga 420
 attcacgctt catacgggtca acgatgatgt cgagggtcag ttcgccatac ccgcgatgat 480
 ggctgggtag attcttcgtc agtccataca cggnaagacg ggtcttnttt agccagacgg 540
 gccagagnca gacccatttt tttctggcag ctttggnntc ggtcaactgc gatggaaata 600
 cccggctcaa ggaattcata cgtttcanaa tgatcggggc attccgggtc aca 653

<210> 427
 <211> 268
 <212> DNA
 <213> Escherichia coli

<400> 427
 ctttcttaaa gccttcttta aaggcgatag aagcagccag tttaaacgcc agttcagagg 60
 agtcaacgtc atggtaagaa ccgaagtgcg gacgaatacc catgtctact accgggtagc 120
 ctgccagcgg acctgctttc agctgttccct ggataccttt atcaacggcc gggatgtatt 180
 cgccagggat tacaccacct ttaatgtcgt tgatgaactc gtagcctttc gggtttgaac 240

ccggctccag cgggtacatg tcgataac

268

<210> 428

<211> 330

<212> DNA

<213> Escherichia coli

<400> 428

gttttgggga	gatgtaaggg	ctaactctgaa	tggctgcatt	ccttggttaa	ggaaaaacga	60
atgactgatt	gccgatacct	gattaaacgg	gtcatcaaaa	tcatcattgc	tgttttacag	120
ctgatccttc	tggtcttata	acacaaggaa	acgtacttaa	ggtgcgtccg	gtgaaccagt	180
cggacgcacc	tttaataact	ataaataagt	gtctgggcag	atactatata	aattaactta	240
gtgaatgatt	atgctaattg	catcaattaa	ataaatataa	tggcgtaaag	gcttcccagt	300
aatataatta	atactctact	tccagagtag				330

<210> 429

<211> 465

<212> DNA

<213> Escherichia coli

<400> 429

gttttgggga	gatgtaaggg	ctaactctgaa	tggctgcatt	ccttggttaa	ggaaaaacga	60
atgactgatt	gccgatacct	gattaaacgg	gtcatcaaaa	tcatcattgc	tgttttacag	120
ctgatccttc	tggtcttata	acacaaggaa	acgtacttaa	ggtgcgtccg	gtgaaccagt	180
cggacgcacc	tttaataact	ataaataagt	gtctgggcag	atactatata	aattaactta	240
gtgaatgatt	atgctaattg	catcaattaa	ataaatataa	tggcgtaaag	gcttcccagt	300
aatataatta	atactctact	tccagagtag	aatattaaat	tttatccgcg	tggtgcatca	360
gcacaaattt	atcccacaac	tggtcttctg	tctcgacatg	cgccggatct	ttcacaatag	420
tattggggat	cgggcacacc	ttctggcagg	ttggtgtctc	gtagt		465

<210> 430

<211> 379

<212> DNA

<213> Escherichia coli

<400> 430

aatctgaatg	gctgcattcc	ttgtttaagg	aaaaacgaat	gactgattgc	cgatacctga	60
ttaaacgggt	catcaaaatc	atcattgctg	ttttacagct	gaccccttctg	ttcttataac	120
acaaggaaac	gtacttaagg	tgcgctccgt	gaaccagtcg	gacgcacctt	taataactat	180
aaataagtgt	ctgggcagat	actatataaa	ttaacttagt	gaatgattat	gctaattgtca	240
tcaattaaat	aaatataatg	gcgttaaggc	ttcccagtaa	tataattaat	actctacttc	300
cagagtagaa	tattaaattt	tatccgcgtg	gtgcatcagc	acaaatttat	cccacaactg	360
ttcttctgtc	tcgacatgc					379

<210> 431

<211> 443

<212> DNA

<213> Escherichia coli

<400> 431

aagatgatgt	gatgagaaag	tcaatttgaa	taagacaata	ttaagagcta	aaaaaatgtc	60
aaaaaacact	aaatcaaaaa	ataatggcat	tagaaaaat	aatgcgaaaa	cggaggtgaa	120
attagtttat	ttcaaatgag	gaaaatctcc	cggcgaaaaa	accgggagat	gaaagtgtga	180
tgggtatcaa	ataaacaaca	gaggagaaat	ttttaacgca	gccattcagg	caaatcgttt	240
aatcccattg	cctggcggat	aagttgcggc	ttaacgccag	gaagcgtgtc	ggccagtttc	300
aaaccaatat	cacgcagcag	ttttttcgcc	ggatttgtac	cggaaaacag	atcgcggaat	360
ccctgcatac	cagccagcat	caacgccgca	ctgtgcttgc	ggctacgctc	atagcgacgc	420

agataaatgt actgcccgat gtc

443

<210> 432

<211> 638

<212> DNA

<213> Escherichia coli

<400> 432

caggggggttt	gttgtgggca	atgatgcatt	taagttatcg	tctgcagata	gaggagatat	60
tacaataaac	aacgaatcag	ggcatttgat	agtcaatacc	gcaattctat	caggagatat	120
agtcactcta	agaggaggag	aaattagggt	ggtattatag	cttgtgcgcg	ccatgattgg	180
cgcgcaattt	aaacttagtg	ctttacatcg	ctattgtctt	gatttccttg	aattatttta	240
taaattaaaa	aaacgactgt	tatgtataag	caaagggtccg	aacgaaaaat	acattccaaa	300
taaattgcttg	cttaaatctc	tatatccttc	cccgaataat	gacacataaa	attgagatat	360
tccaaaaaga	gatactacaa	ataaagatgc	ctttatttta	ttatttctaa	taaaaataga	420
agcaataaaa	aataataaca	atgatataaa	tctaattgtt	ttaaatata	tgtcttttat	480
gtagtaata	gtcgtagta	tggttgattc	tccatatatt	acgtgtagtt	ttttatatac	540
atggaaataa	ttttctttat	actgagacat	cacaccatca	tcaaattggaa	gtttgaagat	600
ggtgcttggt	ttgctaacca	ataaaaagag	tgcattcg			638

<210> 433

<211> 299

<212> DNA

<213> Escherichia coli

<400> 433

ctttacctgg	catgatccac	ttcgccagaa	taccggcaat	aagcccaaaa	ataatccatg	60
acagaatgcc	cattgtttcc	tcacttatct	gttttgcat	agcgggtag	tcgctgataa	120
aaagcatagc	acaacatcgg	gagggcaaga	tttgtgacga	gcacacgga	ggtttttttg	180
cgatggcgca	gaaattgcgc	catcaacgat	cagtgataat	taccaaccac	aaacatcatg	240
ttcgttttcc	gtgtcataag	aacgtacggt	attcaccaga	tcttttatca	cttcagccg	299

<210> 434

<211> 388

<212> DNA

<213> Escherichia coli

<400> 434

gaaaaaggag	gcaatatcgg	gtaaaggcat	tagcccgacg	aatacgtcgg	gctacaaata	60
ttattgtgct	gcaggtgttt	tagcgggttg	ttgatccaca	ggttctaact	ggaagaccac	120
atcgacctga	tcatcaaact	gaatagcggc	ctgctcgtaa	gtttcctggg	cggacaccgg	180
cgcggcatcg	gctttcatca	tccgcacat	tgggctgggc	tgatagttgg	aaacatggta	240
gcgcacgcta	tataccggcc	ccagttttacg	atgaaagccg	ttcgccagtt	cctgcgcctg	300
atgaatcgcg	ttatcaatcg	ctgccttacg	cgctttgtct	ttataggcat	ccggctgcgc	360
cacgcccagc	gacacagaac	gaattccc				388

<210> 435

<211> 351

<212> DNA

<213> Escherichia coli

<400> 435

ctatccttga	tgaaaccgcg	agcaaagata	ggtgattacg	tcatggtttt	acagaaaatt	60
acagaaaaag	gaggcaatat	cgggtaaagg	cattagcccc	acgaatacgt	cgggctacaa	120
atattattgt	gctgcaggtg	ttttagcggg	ttgttgatcc	acaggttcta	actggaagac	180
cacatcgacc	tgatcatcaa	actgaatagc	ggcctgctcg	taagtttctt	gggcggacac	240
cggcgcgcca	tcggctttca	tcatccgcac	cattgggctg	ggctgatagt	tggaacatg	300

gtagcgcacg ctatataccg gccccagttt acgatgaaag ccgttcgcca g 351

<210> 436
 <211> 762
 <212> DNA
 <213> Escherichia coli

<220>
 <221> misc_feature
 <222> (1)...(762)
 <223> n = A,T,C or G

<400> 436
 aattatgaaa cactgtctgg aatcgtctga atgacgggca catttgcgag cacgcatcca 60
 gtaataaacac aggaaactat tttatctacg cgttagcgat agactgcttg catggcgaaa 120
 ggaggtaagc cgacgatttc agcgggacgc tgaaacggga aagcccctcc cgagggaagg 180
 gccataaata aggaaagggt catgatgaag ctactcatca tcgtggtgct cttagtcata 240
 agcttccccg cttactaaga ctaccagggc gggggaaacc ccgctctacc ctcaactctg 300
 aaagtatgcc ttcacgataa gattgtcaat ccgcaggctt tgtagtctgc gatcctgcca 360
 gcaaatattc tttgcgagtc gttacgcaat aatcacagag gaaactatct tattcacgcg 420
 ttagcgatag actgcattca gggcgaaagg aggtgaagccg atgatttcag cgggacgctg 480
 aaacgggaaa gcctctcccc gagaagaggg cttttaataa ggaaagggtt atgatgaagc 540
 acgtcatcat actggtgata ctcttagtga ttagcttcca ggcttactaa gaacaccagg 600
 gggaggggga aacctcttcc taaccctcac ttctgaaatt gggtgctatg acgctggcgt 660
 tactgcttan cgctaccagt ttgtctgccc tggcggttgt aacgccagat cggtagccgt 720
 ttggatattt taatgaaagc cgacaaatca atcancgtga cg 762

<210> 437
 <211> 292
 <212> DNA
 <213> Escherichia coli

<400> 437
 cacatttgcg agcacgcatt cagtaataac acaggaaaact attttatctc cgcgttagcg 60
 atagactgct tgcatggcga aaggaggtaa gccgacgatt tcagcgggac gctgaaacgg 120
 gaaagcccct cccgaggaag gggccataaa taaggaaagg gtcatgatga agctactcat 180
 catcgtggtg ctcttagtca taagcttccc cgcttactaa gactaccagg gcgggggaaa 240
 ccccgtctca ccctcactcc tgaaagtatg ccttcacgat aagattgtca at 292

<210> 438
 <211> 631
 <212> DNA
 <213> Escherichia coli

<400> 438
 atttacactt tttacgaaat catgggatca ctaacaaaat atcgcttgct agttatattg 60
 tatggcagga aagatatgag actgatatta cagatcccca aagtggagag tttatgacca 120
 ttaaaaaata gatgttgctg ggtgcgcttt tgctggttac cagtgccgcc tgggccgcac 180
 cagccaccgc ggggtcgacc aatacctcgg gaatttctaa gtatgagtta agtagtttca 240
 ttgctgactt taagcatttc aaaccagggg acaccgtacc agaaatgtac cgtaccgatg 300
 agtacaacat taagcagtgg cagttgcgta acctgcccgc gcctgatgcc gggacgcact 360
 ggacctatat ggggtgcgag tacgtgttga tcagcgacac cgacggtaaa atcattaaaag 420
 cctacgacgg ttgagattttt tatcatcgct aaaaaaagcc ccctcatcat gagggggaaa 480
 tgcagacacc ttgttattttt ttattattag ccacttgctc gtcttgcttg ttatttagtcg 540
 tatttcacgt tgattaatgc ggttgccctc agtgcgccag atttaacttt gtttgtatcg 600
 tagacgtagt aactggctgt tatcggaatt g 631

<210> 439
 <211> 566
 <212> DNA
 <213> Escherichia coli

<400> 439
 tatggcagga aagatatgcg actgatatta cagatcccca aagtggagag tttatgacca 60
 ttaaaaataa gatgttgctg ggtgcgcttt tgctggttac cagtgccgcc tgggccgcac 120
 cagccaccgc gggttcgacc aatacctcgg gaatttctaa gtatgagtta agtagtttca 180
 ttgctgactt taagcatttc aaaccagggg acaccgtacc agaaatgtac cgtaccgatg 240
 agtacaacat taagcagtgg cagttgcgta acctgccgcg gcctgatgcc gggacgcaact 300
 ggacctatat gggtggcgcg tacgtgttga tcagcgacac cgacggtaaa atcattaaag 360
 cctacgacgg tgagattttt tatcatcgct aaaaaaagcc ccctcatcat gagggggaaa 420
 tgcagacacc ttgttatttt ttattattag ccacttgctc gtcttgcttg ttattagtcg 480
 tatttcacgt tgattaatgc ggttgcctcc agtgcgccag atttaacttt gtttgtatcg 540
 tagacgtagt aactggctgt atcgaa 566

<210> 440
 <211> 339
 <212> DNA
 <213> Escherichia coli

<400> 440
 cgtattcaca tccttttgat tggtgataac atgcgaatcg gtattatatt tccggttgta 60
 atcttcatta cagcggtcgt attttttagca tggtttttta ttggcggcta tgctgccccg 120
 ggagcataaa gatgaaaaaa acaacgatta ttatgatggg tgtggcgatt attgtcgtac 180
 tcggcactga gctgggatgg tggtaacgtc acctctaaaa aatagcaaag gctgcctgtg 240
 tgcagccttt gtgcaattta agcgttaact tttaatcttc ctgtagataa atagcacgac 300
 aatcgcacca ataacggcaa ccacgaagct gccaaaatt 339

<210> 441
 <211> 376
 <212> DNA
 <213> Escherichia coli

<400> 441
 catgaatatt taaaaaggaa aacgacatga aaccgaagca cagaatcaac attctccaat 60
 cataaaatat ttccgtggag cattttatta ttgaatatag aggtttaact ccggtaaaaa 120
 acaaagaagc attgaatgca gggaaaaata atatggccat aaaaaacatc gaaagaaact 180
 cttttaattt aacatgtaaa cgcatggtta atcctcatat cacgggtgga gtgttaagaa 240
 catacataaa tggagtcatg ttttcccttt tccatttatc aagttcctgt tgccgtttta 300
 gtccatctct aattgcatat ttttaatttt ctgataaatg gcattgagca tcgatttcat 360
 ttaaaacaac tgtaca 376

<210> 442
 <211> 446
 <212> DNA
 <213> Escherichia coli

<400> 442
 ttacgatagc tattagtaaa aatataagag ttagctgtat tgttatgtct gtggcgaaat 60
 tgactacctt cgtttttttg attaagaatg atttttattat cgtaagtaaa attacatgaa 120
 tattttaaaaa ggaaaacgac atgaaaccga agcacagaat caacattctc caatcataaa 180
 atattttccgt ggagcatttt attattgaat atagaggttt aactccggta aaaaacaaag 240
 aagcattgaa tgcagggaaa aataatatgg ccataaaaaa catcgaaaga aactctttta 300
 atttaacatg taaacgcatg gttaatcctc atatcacggg tggagtgtta agaacatata 360
 taaatggagt catgttttcc cttttccatt tatcaagttc ctgttgccgt ttttagtccat 420

ctctaattgc atattttaat ttttct

446

<210> 443

<211> 388

<212> DNA

<213> Escherichia coli

<220>

<221> misc_feature

<222> (1)...(388)

<223> n = A,T,C or G

<400> 443

tcaccccggt	gccgattttc	aggcatcctg	atttaactta	gcacccgcaa	cttaactaca	60
ggaaaacaaa	gagataaatg	tctaatacctg	atgcaaatacg	agccgatttt	ttaatcttta	120
cggactttta	cccgcctggt	ttattaattg	caactgtatc	cgccgcttcg	cccgccttta	180
tcacaatagg	ctgtgtagcc	tgggcctggt	tctctttcac	ccgcgccaga	gcggcagcaa	240
tcgcatcttt	atctttggct	gcagggtgaa	cggctgcgct	cttatgtcgt	tcaaggcgag	300
ccgctttttc	gcgctccaga	cgagcctggc	gcgcttcgaa	acgcgctttg	gcttctgcgg	360
cncgcttttc	ttcctgacga	atagccgc				388

<210> 444

<211> 209

<212> DNA

<213> Escherichia coli

<400> 444

aattttaata	acgctatctg	cggataaagc	agaatagggtg	gttaacccca	gacataaacc	60
gaggaaaata	atgttattgt	atttcataat	ctattgttcc	ttagcgacag	attgctgtct	120
gctgggtcag	taaggtagca	ggagaaactt	caggaagctt	gtactcgaca	atacagtttg	180
agtttttatc	tttgcccat	gaaacctgt				209

<210> 445

<211> 341

<212> DNA

<213> Escherichia coli

<400> 445

catcctcaat	accgttaaat	gcaacccgaa	cccccggtgt	ccctttgctg	cattcaacta	60
acgtaatctg	aaaaggagcg	gctggacttg	tgctaccggt	cggttgaaat	tgtctggcac	120
tggttttttg	gagatctacg	gtaaaattaa	gcgaatccga	tgagactgtg	cagccataat	180
cgaggacgcg	cccgcataat	ttaataacgc	tatctgcgga	taaagcagaa	taggtgggta	240
acccagaca	taaaccgagg	aaaataatgt	tattgtattt	cataatctat	tggttccttag	300
cgacagattg	ctgtctgctg	gttcagtaag	gtaccaggag	a		341

<210> 446

<211> 697

<212> DNA

<213> Escherichia coli

<400> 446

agatttactg	ccaatttccg	gcagatcgga	aagggttaam	ccatattgat	ccataagggt	60
acgaatcmcg	ggctataccg	ccaggcatgg	cttgagccat	ggcattaaat	tccgcaaatt	120
cgggcgctga	ttcttcccac	gcggttattt	tggcacacac	cagatccagc	aagggggttt	180
caggatcggt	gagcagcaga	tgatctacca	gttccagcgc	ctgggtgtat	tggtcctcgt	240
tctgaatacc	cgccagaaaa	ggtgccacag	cagttagctt	ttctcctgct	tgcaagatgt	300
cggcaatcgc	aatcattttt	tccccttagt	acgatgaaca	gcggtaaaga	aatcgtattc	360

tttatg	cgctc	ataact	tcac	gtatgt	tagca	cttttg	cgat	tcaaaaa	aaga	ccattg	ctac	420
aacacg	taaat	tcattg	cccc	caacatt	gaa	aacata	atgc	ttatcc	cagat	atttga	agtt	480
atccag	agat	gggaata	ctg	ctttta	atga	ctcagg	tttt	ttgaaat	atc	ccttag	caat	540
cg	gtkcccc	agagcc	acca	actccg	tttt	atgttg	cg	tattttt	ccg	cagcat	cttt	600
caatg	ctttt	tgagtt	atca	ggtgc	attct	tc	atcacg	tc	g	kgmcaaa	ttgg	660
gataac	atcc	g	ttgcc	cagat	tg	gcac	ggat	ga	attat			697

<210> 447
 <211> 215
 <212> DNA
 <213> Escherichia coli

<400> 447												
aattaataac	ttttcg	ttag	gcag	ttttg	gtgtg	agttg	caagag	ggga	gactact	gaa	60	
taactcaagt	tttata	atcg	agggg	aaaat	ggtgat	ggcg	ttcatag	caa	aacgc	cctca	120	
accataaagg	tcgagg	gcgc	ttaag	atg	tt	aaaa	accgc	tatccg	ttaa	aaaaca	atgt	180
tcaactaagg	tcagtg	acat	tg	cgct	aaaa	aagcg					215	

<210> 448
 <211> 395
 <212> DNA
 <213> Escherichia coli

<400> 448											
gcattattca	tgagaa	atgt	gtatcg	taaa	tcaact	gaaa	ttaacg	caac	catttg	ttat	60
ttaagg	ttta	attatc	tgtg	atattt	tattga	aatgt	tttaa	atatt	gttttt	tattg	120
gcattg	ctat	aatatt	gg	atcatt	tg	ct	ag	tt	ag	tt	180
taaggg	acag	gc	atag	ag	ta	atgata	cg	ta	tg	ca	240
attgaat	g	tt	g	at	g	g	g	g	g	g	300
aaattc	at	at	g	gc	ct	tg	ct	at	g	aa	360
atattg	aa	at	g	ca	acta	ctt	ct	tt	tatt	ac	395

<210> 449
 <211> 641
 <212> DNA
 <213> Escherichia coli

<220>
 <221> misc_feature
 <222> (1)...(641)
 <223> n = A,T,C or G

<400> 449																	
ataatc	aggt	aagaaa	aggt	gcgcg	gagat	taccgt	gtgt	tg	cgat	atat	tttttag	ttt	60				
cg	cg	tg	gg	caa	tacat	cag	tg	gcaata	aaaac	gacata	tcca	gaaaa	atata	cacta	ag	120	
at	gata	tctt	ccgatt	tatc	ttaat	cgttt	atgg	ataacg	gcaa	aggg	ct	tcg	tttttt	tc		180	
ctata	cttat	tcag	cactca	caaata	aaag	aacg	ccaatg	aaaatt	tatac	tctg	ggg	ctgt				240	
attg	attatt	ttcct	gattg	ggct	actgg	ggtg	actggc	gtatt	taaga	tgat	atttt	ta				300	
aaatta	atta	atgt	catcag	gtcc	gaaa	aat	aacg	aga	ata	ttcag	tctc	tc	atc	cctg	tt	360	
gcg	ctc	ctgt	catgt	gcatt	gctt	catata	atcact	ggcg	caagg	agcg	cgcag	gcg	na			420	
gnntg	cn	cg	n	cg	n	cg	n	cg	n	cg	n	cg	n	cg	n	cg	480
cgat	ng	tcg	cg	gg	ng	cctc	cccat	gc	nan	agtang	gg	aa	ntg	ccang	cg	ncnnatt	540
cgaa	agg	ctn	attn	caa	aga	ctgg	gc	cttn	cnttt	at	ctg					600	
tcctg	agnan	gacaa	atncc	gccg	ggg	agcg	gattt	ga	acn	t						641	

<210> 450
 <211> 314

<212> DNA
<213> Escherichia coli

<220>
<221> misc_feature
<222> (1)...(314)
<223> n = A,T,C or G

<400> 450
gaactacgag taagaatagc tncgaattcc cgtttatgga taacggcaaa gggcttcggt 60
ttttcctata cttattcagc actcacaaat aaaggaacgc caatgaaaat tatactctgg 120
gctgtattga ttattttcct gattgggcta ctgggtggtga ctggcgatt taagatgata 180
ttttaaaatt aattaatgtc atcaggtccg aaaataacga gaatatttca gtctctcatc 240
ctgttgcgct cctgtcatgt gcattgcttc atataatcac tggcgcaagg agcgcgagg 300
gggntntnnt cttt 314

<210> 451
<211> 236
<212> DNA
<213> Escherichia coli

<400> 451
atatacacta agtgaatgat atcttccgat ttatcttaat cgtttatgga taacggcaaa 60
gggcttcggt ttttcctata cttattcagc actcacaaat aaaggaacgc caatgaaaat 120
tatactctgg gctgtattga ttattttcct gattgggcta ctgggtggtga ctggcgatt 180
taagatgata ttttaaaatt aattaatgtc atcaggtccg aaaataacga gaatat 236

<210> 452
<211> 418
<212> DNA
<213> Escherichia coli

<400> 452
cggagattac cgtgtgttgc gatatatattt ttagtttcgc gtggcaatac atcagtggca 60
ataaaacgac atatccagaa aaatatacac taagtgaatg atatcttccg atttatctta 120
atcgtttatg gataacggca aagggtctcg ttttttcta tacttattca gcactcacia 180
ataaaggaac gccaatgaaa attatactct gggctgtatt gattattttc ctgattgggc 240
tactggtggt gactggcgta tttaagatga ttttttaaaa ttaattaatg tcatcaggtc 300
cgaaaataac gagaatattt cagtctctca tcctgttgcg ctctgtcat gtgcattgct 360
tcatataatc actggcgcaa ggagcgcgca gggggcgggc aatcgccgcc gccccctg 418

<210> 453
<211> 551
<212> DNA
<213> Escherichia coli

<400> 453
aacaatttgc ccatgcgctc ggtcatgcgc tgcacgccc ggccattttg sgcgctccccg 60
cgaccgccat tcgactgtta atgggcgaat cttcagtact ggtattaggt ggacaacgcg 120
cgctgcctaa acggctggaa gaagcgggtt ttgcgtttcg ctggtacgat ttagaagagg 180
cgctggcgga tgctgttcgc tgatgtggtt tacagcaaac atccgccagt taactcccgg 240
tgttacagga ttagtggctt tgcgcgataa gatcgtctgg tgaaagtcgg gtcaccatca 300
taactaactc tctgtctaaa cctctatcca gcatctcctg agcaatacgc agggcttctt 360
cgtgttttgc ctgcattgcg ccttcttcac gtaatctgtc agcaatggtc atcaagtttc 420
tccttttctt gtgggtgcgcg ttccgctatc tcaccaataa atgcacgaaa acgctgggca 480
tcccctgttt gtaatacgta attaaacagg gcttttagct gtctgtcatt agtgktccct 540
gtaactagca g 551

<210> 454
 <211> 93
 <212> DNA
 <213> Escherichia coli

<400> 454
 tggcatctcg gtgttgccga tcttcatgat atccagcccg ccggaactt cttcccaaac 60
 ggttttgctg ttatccattg agtcacggaa ctg 93

<210> 455
 <211> 232
 <212> DNA
 <213> Escherichia coli

<400> 455
 cgtgccgaga tgatcctgta accatcatca gttgtgaagt agtgattcac gacttcaagg 60
 cgcttttcaa aagggtatgt tggctttgac atattagggg ctattccatt tcatcgcca 120
 acaaaatggg tgcagtacat actcgttggg aatcaacaca ggaggctggg aatgccgcag 180
 aaatatagat tactttcttt aatagtgatt tgtttcacgc ttttattttt ca 232

<210> 456
 <211> 713
 <212> DNA
 <213> Escherichia coli

<220>
 <221> misc_feature
 <222> (1)...(713)
 <223> n = A,T,C or G

<400> 456
 ttagnggatn naangccac ancctcgang gatctaggag gtagaatagc ttcgaattcc 60
 ccagcagagc gcggccttct tcgtcagatt tcgcagtagt ggtaatggta atatccaaac 120
 cacgaacgag gtcgacttta tcgtagtcga tttctgggaa gatgatctgc tcacggacac 180
 ccatgctgta gttaccacga ccgtcgaaag acttagcggg caggccacgg aagtcacgga 240
 tacgaggtac agcaatagt atcaggcgct caaagaactc ccacatgcgt tcgccacgca 300
 gagttacttt acagccgatc ggatagccct gacggatttt gaagcctgca acagatttgc 360
 gtgctttggg gatcagcggg ttttgaccgg agattgctgc caggctctgct gctgcgttat 420
 ccagcagttt tttgtcagcg atcgtttcac caacacccat gttcagggtg atcttctcga 480
 cccgagggac ttgcatgaca gaattgtagt taaactcagt catgagtttt ttaactactt 540
 cgtctttgta gtaatcatgc agtttcgcca tcgtactact ccatgtcggg gaacgctctc 600
 ctgagtagga caaatccgcc ggagccggat ttaacgttgc gaacaaccgn cccggagggg 660
 tggnggcagg accccgccat aactggcagc attaaattaa gcagaaggcc atc 713

<210> 457
 <211> 292
 <212> DNA
 <213> Escherichia coli

<400> 457
 tgaacagcag agatacggcc agtgccggcca atgttttttg tccttttaaac ataacagagt 60
 ccttttaagga tatagaatag gggatatagct acgccagaat atcgtatttg attattgcta 120
 gtttttagtt ttgcttaaaa atattgttag ttttattaaa tgcaaaacta aattattggg 180
 atcatgaatt tgttgatga tgaataaaat ataggggggt atagatagac gtcattttca 240
 taggggttata aatgcgacta ccatgaagtt ttttaattgaa agtattgggt tg 292

<210> 458
 <211> 282
 <212> DNA
 <213> Escherichia coli

<400> 458
 ttattaaatg caaaactaaa ttattggtat catgaatttg ttgtatgatg aataaaatat 60
 aggggggtat agatagacgt cattttcata ggggtataaa tgcgactacc atgaagtttt 120
 taattgaaag tattgggttg ctgataattt gagctgttct attcttttta aatatctata 180
 taggtctgtt aatggatttt atttttacaa ttttttgtgt ttaggcataat aaaaatcaac 240
 ccgccatatg aacggcgggt taaaatattt acaacttagc aa 282

<210> 459
 <211> 300
 <212> DNA
 <213> Escherichia coli

<400> 459
 tctgcgttcc gctaaaaggt gcaaatgctc aggacgttgc agcgttttgc gtgaccgctc 60
 ggggaaggca aaattgcctc tgggaaagca ttgcgcgggg tccggcgctc atcaacaatc 120
 ggggggcagc aaggggctga aacgggaaaag cccctcccga agaaggggcc ttgtataagg 180
 aaagggttat gatgaagctc gtcatactac tgggttgtgt gttactgtta agtttcccga 240
 cttactaaca actcatcaga ggggggagaa atcctccctt acccttgctc cttactcta 300

<210> 460
 <211> 293
 <212> DNA
 <213> Escherichia coli

<400> 460
 cgggggtccg cgctcatcaa caatcggggg gcagcaaggg gctgaaacgg gaaagcccct 60
 cccgaagaag gggccttgta taaggaaagg gttatgatga agctcgtcat catactggtt 120
 gtgttggtac tgtaagttt cccgacttac taacaactca tcagaggggg gagaaatcct 180
 cccttaccct tgttccttta ctctagggtg aaaaaacaac agcgtcaata ggcctgccat 240
 gtacgaagcg agatctgtga accgctttcc ggtagcctt ttttatcctg ttg 293

<210> 461
 <211> 359
 <212> DNA
 <213> Escherichia coli

<400> 461
 caacacagga ggctgggaat gccgcagaaa tatagattac tttctttaat agtgatttgt 60
 ttcacgcttt tatttttcac ctggatgata agagattcac tgtgtgaatt gcatattaaa 120
 caggagagtt atgagctggc ggcgttttta gcctgcaaat tgaaagagta agagtcttcg 180
 gcgggaaatt attccgcct tacttacggc gttgcgcatt ctattgcac ccaaatttat 240
 tcttcacaaa aataataata gattttatta cgcgatcgat tattttattc ctgaaaacaa 300
 ataaaaaat ccccgccaaa tggcagggat cttagattct gtgcttttaa gcagagatt 359

<210> 462
 <211> 673
 <212> DNA
 <213> Escherichia coli

<400> 462
 gcaacccatg tcttgacctg ggttcggggg acacaaaaac gtgccgagat gatcctgtaa 60
 ccatcatcag ttgtgaagta gtgattcacg acttcaaggc gcttttcaaa agggattttt 120

ggctttgaca	tattaggggc	tattccattt	catcgtccaa	caaaatgggt	gcagtacata	180
ctcgttgga	atcaacacag	gaggctggga	atgccgcaga	aatatagatt	actttcttta	240
atagtgttt	gtttcacgct	tttatttttc	acctggatga	taagagattc	actgtgtgaa	300
ttgcatatta	aacaggagag	ttatgagctg	gcggcgtttt	tagcctgcaa	attgaaagag	360
taagagtctt	cggcgggaaa	ttattcccgc	cttacttacg	gcgttgcgca	ttctcattgc	420
acccaaattt	attcttcaca	aaaataataa	tagattttat	tacgcgatcg	attattttatt	480
tcctgaaaac	aaataaaaaa	atccccgcc	aatggcaggg	atcttagatt	ctgtgctttt	540
aagcagagaa	tacaggctgg	ttacgttacc	agctgccggg	cctttagcgc	cgctttcgat	600
ggtgaaggac	actttctgac	cttcgtccag	agatttgtaa	ccatcgttct	ggatagcaga	660
gaagtgtacg	aac					673

<210> 463

<211> 630

<212> DNA

<213> Escherichia coli

<400> 463

tggtggcatt	ggttgctgga	gagagaaaac	ccccgcacgt	tgcaggtatg	cacctgacaa	60
caccacgggg	gctaactctg	actctagacc	actcaagaat	agccgcgaaa	cgttgtcatt	120
acaacacagg	cggctatatg	acgttcgcag	agctgggcat	ggccttctgg	catgatttag	180
cggctccggt	cattgctggc	attcttgcca	gtatgatcgt	gaactggctg	aacaagcgga	240
agtaacgtgt	catgcgggcg	tcaggctgcc	gtaatggcaa	tttgcgccc	gaccaggccg	300
caggggggaa	actctgcggc	ctttttcggt	cttactgcgg	gtaaggcacc	cagtcgccgc	360
cgttcaggcg	aacgtacggt	ttatcctggt	attgaataac	tactgcattt	gagttctcgg	420
agaccggtgc	tgtttggtgc	aaccactg	tgagtttttt	ccagtcaaca	ttgtcttcgg	480
tgaaaatcct	gccatcgaga	acgcgaacca	ccagatcgga	gatagccagg	aagctgctcg	540
gttggttcgat	gacaatcggg	gccccctgat	gcggtgcctt	catgccgaag	aatttcaccc	600
caacggggac	gtcgggtgata	gacgggctag				630

<210> 464

<211> 391

<212> DNA

<213> Escherichia coli

<400> 464

ctcaggctgc	tgattgtttt	tttgtgcaat	ggcgcggtat	tagcgtcggt	gctgtcgatg	60
gagagaatca	taaactgtgt	gaatgatgat	tgtagcaag	gaaaactgtc	aaaaatcttc	120
aaaaaatttg	agggataagg	ccggaatggc	tccggccaga	gggaagttaa	ccgcgaagct	180
gttgctgctt	gagggctcgt	ttaaccagac	gccaggcgct	ccatacgcca	aaaccgcgtc	240
tgcccagcg	gaccagcata	ttaggatggc	gaatcgcca	gatcgccatc	acgctactgc	300
caaccagcgc	ccaggagcgc	agacttagca	gcatattcca	gcgacgatcg	taagcgcctg	360
ttgtctccag	ccattcacga	cgactggcgg	a			391

<210> 465

<211> 625

<212> DNA

<213> Escherichia coli

<400> 465

aacacaccac	accataaacg	gaggcaaata	atgctgggta	atatgaatgt	tttaatggcc	60
gtactgggaa	taattttatt	ttctggtttt	ctggccgcgt	atttcagcca	caaatgggat	120
gactaatgaa	cggagataat	ccctcaccta	accggcccct	tgttacagtt	gtgtacaagg	180
ggcctgattt	ttatgacggc	gaaaaaaaac	cgccagtaaa	ccggcggtga	atgcttgcatt	240
ggatagattt	gtgttttgct	tttacgctaa	caggcatttt	cctgcactga	taacgaatcg	300
ttgacacagt	agcatcagtt	ttctcaatga	atgttaaacg	gagcttaaac	tcggttaatc	360
acattttgtt	cgtcaataaa	catgcagcga	tttcttcggg	tttgcttacc	ctcatacatt	420
gcccggtccg	ctcttccaat	gaccacatcc	agaggctctt	caggaaatgc	gcgactcaca	480

cctgctgtca	cggtaatgtt	gatatgccct	tcagaatgtg	tgatggcatg	gttatcgact	540
aactggcaaa	ttctgacacc	tgacagacat	gcttcttcat	cattagccgc	tttgacaata	600
atgataaatt	cttcgcccc	gtagc				625

<210> 466
 <211> 623
 <212> DNA
 <213> Escherichia coli

<400> 466						
tgcttttgaa	tatgtgctcg	caatcttgag	aaggaaatgg	cgaccacgaa	agaaaaggca	60
aaaacgataa	tctgaaagag	ccaaggtatt	tcagtataag	cattgaatgc	gacagtaaac	120
tctttcggta	tcagccagag	agtgcagcca	aaaatgataa	tcgtatacat	aagtccttcg	180
agtggctcgt	tagcaaaaag	tttcaacaat	ggagtaaata	catccaacat	atcaataact	240
ctcaactgta	agggtattga	aatgttaaca	caagctctcg	ctgtaggggt	atagccgaga	300
ccaccgaagc	ccggagggtg	tgaaataaaa	ccgggcacaa	cacgaaggcg	catttccgat	360
atccataaag	agtcggtctt	gtctgttaaa	tttaaatggt	gggagtgcgc	ctccggttgt	420
aaataacgac	attgctgtgt	gtagtcctgg	cggcatcagt	ttttttcttg	aagttcggct	480
gatgtccgcc	ctttttaaag	tgaattttgt	gatgcggtga	atgcggctaa	gcgcacgtgg	540
cacagttaaa	agtcatgtta	gtccttattg	gtttgggtgg	gaaagccgac	tgtaattgtt	600
aactggttgc	agtcacctgg	agg				623

<210> 467
 <211> 234
 <212> DNA
 <213> Escherichia coli

<400> 467						
tgtttactta	caagagattc	atctttgtat	aaataaagat	aagtaattac	gcataaaaca	60
acaatgatta	taatagcaaa	aataaatatt	atcatctttg	atagattact	tgagatagcc	120
agcatcttgt	aaagccttta	tcgttttttt	atgctctgga	ttaatataat	cactacatct	180
atctgagcaa	tctgtttgtg	atggacatgt	caaccatgg	tcatttacag	ccaa	234

<210> 468
 <211> 529
 <212> DNA
 <213> Escherichia coli

<400> 468						
attagctatt	tcggctaaaa	tagagactac	atgtcttcgg	tccatctcac	ttaaggagtg	60
tagttccggt	gtaagttttt	ccatagcttg	cactgctaaa	tttcgaacaa	ggaattttct	120
gctggtaatc	tctaaaaaga	tggtatggtt	tacaatgatt	tttgtttcct	tttgattatt	180
atgaacaact	gtccatgatt	tcgtttaaga	atgaagagaa	atcactaaac	gaactgaata	240
tattttctgt	gccaatatta	tctctaattt	caaaaaagtt	acttttaatg	tcggtaatga	300
ctccaactta	ttgatagtgt	tttatgttca	gataatgcc	gatgactttg	tcatgcagct	360
ccaccgattt	tgagaacgac	agcgacttcc	gtcccagccg	tgccagggtg	tgccctcagat	420
tcaggttatg	ccgctcaatt	cgctgcgtat	atcgcttttc	cttatcagtt	cgttgatgtc	480
agtggttttg	accacgaggg	agcttcacgc	gagttattga	aaaccctga		529

<210> 469
 <211> 261
 <212> DNA
 <213> Escherichia coli

<400> 469						
caaagaacct	tcaacatgaa	aaatatccat	ttgtttgcaa	aaaaagatta	ttaggaagga	60
aattaatgca	attatcgaaa	attcaaaaaa	tatccaaaaa	tagtatactt	tattccagaa	120

gagttcaata taatgtttgt cttcaatfff tcttacttca gggtaatata gattgctcat	180
tacattgtga gcttcatctt tatttaattt tctgttgact ccagctctcc gtgataacgg	240
ttttataatt agatgcttat c	261

<210> 470
 <211> 98
 <212> DNA
 <213> Escherichia coli

<400> 470	
agatgattgc cgggaacttg ttagcggcac gcaggcggcg gctcgcaccc ttaccctgct	60
ctttacgtac ttctgcgttg atagtaaaca tttctttc	98

<210> 471
 <211> 259
 <212> DNA
 <213> Escherichia coli

<400> 471	
agcgcgaacg aagtcgatgt gctgcagctt cggtttgtac gggtgacgct gtacgtcctg	60
agctttaact ttgatttctt taccgtcaac aacgatggtc agaacttcgc tgtagaattc	120
agcttttagct tgcattgtca tgactttgtc gtgatccagc tcgatagcca gcggcgcttc	180
tttgccaccg tagatgattg ccgggaactt gtttagcggca cgcaggcggc ggctcgcacc	240
cttaccctgc tctttacgt	259

<210> 472
 <211> 94
 <212> DNA
 <213> Escherichia coli

<400> 472	
aaaaacggcg taaagaaagg atgcaaacat gtttaataaaa actcaaattg atcccacgta	60
tatattacgc cgcaaaatcc ttacaataaa cagg	94

<210> 473
 <211> 174
 <212> DNA
 <213> Escherichia coli

<400> 473	
ttaattatta aaatagtgtg acgcgattat gtggttatgg gggtaaacad taaataaacc	60
agcggggagg ggaggtaaag tgaaaaaata aaaagcggat aatcttaata agcaggccgg	120
acagcatcgc catccggcac tgatacgagg tttatttcag ctcatcaacc atcg	174

<210> 474
 <211> 138
 <212> DNA
 <213> Escherichia coli

<400> 474	
ctgtaaaaac gtcaaaaaga gtgtttttatc aacagaagaa tggaggctctg acagatagta	60
gtaatgcaaa aaaatggaga cttaagttga atgaacggga gtaaagcgaa aagactatag	120
agtgaaggag aaattccc	138

<210> 475
 <211> 191
 <212> DNA

<213> Escherichia coli

<400> 475

tttgttggct	taatattcta	ttgttatctt	tatttataga	tgtttatatt	gcatgaggtg	60
gtttttggag	agaagaatga	ggaagatgcg	tcgagccaca	gaaacgttag	ctttacatat	120
agcggaggtg	atgtgaaatt	aatttacaat	agaaataatt	tacatatcaa	acagttagat	180
gctttttgtc	g					191

<210> 476

<211> 245

<212> DNA

<213> Escherichia coli

<400> 476

cggccattta	tacaggaaaa	gcctatgtca	gaacgtaaaa	actcaaaatc	acgccgtaat	60
tatctcgtta	aatgttcctg	cccaaactgc	acccaagagt	cagaacacag	tttttcaaga	120
gtacaaaaag	gtgccctttt	gatctgccct	cattgcaaca	aagtattcca	gacaaatctt	180
aaagctgtag	cctgattgat	tttattagta	acaagtattt	tttatatttt	aataatatat	240
ttaaa						245

<210> 477

<211> 319

<212> DNA

<213> Escherichia coli

<400> 477

aaattttcag	gtaccttgtc	accatacttt	tttttctgag	cattaatgat	attttgagct	60
tcttgaggat	ctttaactcc	ccacatttgg	tggaaagtat	tcatattaaa	aggaaggttg	120
aataatttgt	ctttataaat	cgccagtgga	gaattagtaa	aacgattaaa	ttctactaaa	180
tcattaacgt	aatcccatat	atatttatca	ttggtatgaa	aaatatgtgc	accatattta	240
tgaatctgga	taccctcaca	gtcctctgtg	tacgcatttc	caccgatatg	atttcttttc	300
tcaatcacta	aaacttttt					319

<210> 478

<211> 149

<212> DNA

<213> Escherichia coli

<400> 478

gcagtgatcg	aagcgatgac	gaagtgtatg	gaaaaatcag	aaaaactcag	caaatcctga	60
tgactttcgc	cggacgtcag	gccgccactt	cgggtcgggt	acgtccggct	ttctttgctt	120
tgtaaagcgc	caaatctgcc	gatttcaac				149

<210> 479

<211> 330

<212> DNA

<213> Escherichia coli

<400> 479

gaaagtatct	tcgttattga	catcactgga	aaatataact	tgcttttcat	tattaaactc	60
gaagcgcgta	ccgtatctgg	acaaacattt	atcgagctta	ccaaattcct	gaagaggttt	120
aactacagat	aacatttgcg	cgtcctttgc	agtaatgcc	gtcaaatcct	tgacgggcat	180
tatttagatt	aaattaccag	tatttcttgc	gagtgaagaa	tattaccagg	tatatttaac	240
acccacgttc	gcggaaccgt	cttgatctac	gtcaccacca	ccgaggtagt	tagcatcggt	300
ataggcgctg	aagttcttgg	tgaagctaaa				330

<210> 480

<211> 191
 <212> DNA
 <213> Escherichia coli

<400> 480
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